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OM protein - protein search, using sw model

Run on: March 14, 2003, 19:21:19 ; Search time 25 Seconds
(without alignments)
549,620 Million cell updates/sec

Title: US-09-689-159A-2
Perfect score: 2391
Sequence: 1 MTELPAPPLSYFQNAQMSQEDN.....ATDYLVQPFMDQLAFHQFYI 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Sequence
1	2391	100.0	467	2	US-08-967-101-2
2	2391	100.0	467	2	US-08-592-541-2
3	2391	100.0	467	3	US-09-124-698-2
4	2391	100.0	467	4	US-09-127-480-2
5	2391	100.0	467	4	US-08-486-841C-2
6	2391	100.0	467	4	US-09-124-523-2
7	2387	99.8	467	2	US-08-967-101-134
8	2387	99.8	467	2	US-08-592-541-134
9	2387	99.8	467	3	US-08-923-454A-10
10	2387	99.8	467	3	US-08-670-964-2
11	2387	99.8	467	3	US-08-888-077A-2
12	2387	99.8	467	3	US-08-124-698-134
13	2387	99.8	467	4	US-09-127-480-134
14	2387	99.8	467	4	US-08-486-841C-134
15	2387	99.8	467	4	US-08-832-867-3
16	2387	99.8	467	4	US-09-227-725A-1
17	2387	99.8	467	4	US-09-124-523-134
18	2387	99.8	467	4	US-08-375-318-3
19	2387	99.6	467	4	US-08-706-344C-2
20	2377	99.4	467	4	US-08-706-344C-32
21	2370	99.2	467	4	US-08-706-344C-30
22	2370	99.1	467	4	US-08-706-344C-28
23	2361	98.7	463	3	US-08-888-077A-4
24	2357	98.6	463	3	US-08-670-964-4
25	2355	98.5	467	4	US-08-706-344C-4
26	2334	97.6	463	2	US-08-670-479-18
27	2300	96.2	462	3	US-08-788-231A-15

28	2237	93.6	467	3	US-08-888-077A-17	Sequence 17, Appl
29	2237	93.6	467	4	US-08-496-841C-136	Sequence 136, App
30	2190	91.6	467	2	US-08-967-101-4	Sequence 4, Appl
31	2190	91.6	467	2	US-08-592-541-4	Sequence 4, Appl
32	2190	91.6	467	3	US-09-124-698-4	Sequence 4, Appl
33	2190	91.6	467	4	US-09-127-480-4	Sequence 4, Appl
34	2190	91.6	467	4	US-08-486-841C-4	Sequence 4, Appl
35	2190	91.6	467	4	US-09-124-523-4	Sequence 4, Appl
36	2183.5	91.3	465	3	US-08-788-231A-17	Sequence 17, Appl
37	2066	86.4	407	2	US-08-875-972-4	Sequence 4, Appl
38	1461	61.1	448	2	US-08-967-101-137	Sequence 137, App
39	1461	61.1	448	2	US-08-592-541-137	Sequence 137, App
40	1461	61.1	448	3	US-08-888-077A-19	Sequence 19, Appl
41	1461	61.1	448	3	US-08-124-698-137	Sequence 137, App
42	1461	61.1	448	4	US-09-127-480-137	Sequence 137, App
43	1461	61.1	448	4	US-09-227-725A-2	Sequence 2, Appl
44	1461	61.1	448	4	US-09-124-523-137	Sequence 137, App
45	1461	61.1	448	4	US-09-375-318-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-967-101-2
Sequence 2, Application US/08967101
Patent No. 5840540
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESSES:
ADDRESSEE: TESTA, HORMITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-967-101-2
Query Match 100.0%; Score 2391; DB 2; Length 467;
Best Local Similarity 100.0%; Pred. NO. 9.7e-235;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MTELPAPPLSYFQNAQMSQEDNHLSTVRSQNDNRSLGHPPLSGRPOGNSR 60
|||||

Db 1 MTELAPLSTFQNAQSEDNHLSNTVRSQNDNREQEHNDRLSGHPEPLSNGRPOGNSR 60
QY 61 QVEODEEDELTLKYGAKHVMLEFVPTLCMVVVVATIKSVSEYTRKDGLIYTPFTE 120
Db 61 QVEODEEDELTLKYGAKHVMLEFVPTLCMVVVVATIKSVSEYTRKDGLIYTPFTE 120
QY 121 DTEYVQGRALHSILNAAIMISIVYVMTLLVLYKRCYKVIHAWLIISLLEFFESFI 180
Db 121 DTEYVQGRALHSILNAAIMISIVYVMTLLVLYKRCYKVIHAWLIISLLEFFESFI 180
QY 181 YGVEFKTYNNAVDTITVALLIMNLGVGMISIHMKGPLRLOQAVLIMISALMALVFIKY 240
Db 181 YGVEFKTYNNAVDTITVALLIMNLGVGMISIHMKGPLRLOQAVLIMISALMALVFIKY 240
QY 241 LPEWTAMILIAVISYDVAVLCPRGPLRMLVETAQERNETLFPALISSTWVWLVNNAE 300
Db 241 LPEWTAMILIAVISYDVAVLCPRGPLRMLVETAQERNETLFPALISSTWVWLVNNAE 300
QY 301 GDEPQRRVSKSKYNAESTERESODTYAENDDGFSEMEQORDSHLGPSTPESRAA 360
Db 301 GDEPQRRVSKSKYNAESTERESODTYAENDDGFSEMEQORDSHLGPSTPESRAA 360
QY 361 VOELSSSILAGDPERGVKLGDFIFYSVLYGKASATASGDMWTTTACFAVAILIGLCL 420
Db 361 VOELSSSILAGDPERGVKLGDFIFYSVLYGKASATASGDMWTTTACFAVAILIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGVYFATDYLVPFMDQLAFHQFYI 467
Db 421 TLLLAIFKKALPALPISITFGVYFATDYLVPFMDQLAFHQFYI 467

RESULT 2
US-08-592-541-2
Sequence 2, Application US/08592541
Patent No. 5986054

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESS: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-592-541-2

Query Match 100.0%; Score 2391; DB 2; Length 467;

Best Local Similarity 100.0%; Pred. No. 9.7e-235;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTELAPLSTFQNAQSEDNHLSNTVRSQNDNREQEHNDRLSGHPEPLSNGRPOGNSR 60
Db 1 MTELAPLSTFQNAQSEDNHLSNTVRSQNDNREQEHNDRLSGHPEPLSNGRPOGNSR 60
QY 61 QVEODEEDELTLKYGAKHVMLEFVPTLCMVVVVATIKSVSEYTRKDGLIYTPFTE 120
Db 61 QVEODEEDELTLKYGAKHVMLEFVPTLCMVVVVATIKSVSEYTRKDGLIYTPFTE 120
QY 121 DTEYVQGRALHSILNAAIMISIVYVMTLLVLYKRCYKVIHAWLIISLLEFFESFI 180
Db 121 DTEYVQGRALHSILNAAIMISIVYVMTLLVLYKRCYKVIHAWLIISLLEFFESFI 180
QY 181 YGVEFKTYNNAVDTITVALLIMNLGVGMISIHMKGPLRLOQAVLIMISALMALVFIKY 240
Db 181 YGVEFKTYNNAVDTITVALLIMNLGVGMISIHMKGPLRLOQAVLIMISALMALVFIKY 240
QY 241 LPEWTAMILIAVISYDVAVLCPRGPLRMLVETAQERNETLFPALISSTWVWLVNNAE 300
Db 241 LPEWTAMILIAVISYDVAVLCPRGPLRMLVETAQERNETLFPALISSTWVWLVNNAE 300
QY 301 GDEPQRRVSKSKYNAESTERESODTYAENDDGFSEMEQORDSHLGPSTPESRAA 360
Db 301 GDEPQRRVSKSKYNAESTERESODTYAENDDGFSEMEQORDSHLGPSTPESRAA 360
QY 361 VOELSSSILAGDPERGVKLGDFIFYSVLYGKASATASGDMWTTTACFAVAILIGLCL 420
Db 361 VOELSSSILAGDPERGVKLGDFIFYSVLYGKASATASGDMWTTTACFAVAILIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGVYFATDYLVPFMDQLAFHQFYI 467
Db 421 TLLLAIFKKALPALPISITFGVYFATDYLVPFMDQLAFHQFYI 467

RESULT 3
US-09-124-698-2
Sequence 2, Application US/09124698
Patent No. 6117978

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESS: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-124-698-2

Query Match 100.0%; Score 2391; DB 3; Length 467;
Best Local Similarity 100.0%; Pred. No. 9,7e-235;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSQSDNHLSTNVRSONDREROENHRRSLGHPPELSNGRPOGNSR 60
DB 1 MTELPAPLSYFQNAQMSQSDNHLSTNVRSONDREROENHRRSLGHPPELSNGRPOGNSR 60
QY 61 QVVEDEDEDEDELTKYGAHVIMLFVPTLCMVVAVATIKSVSYTRKDGLITPTPE 120
DB 61 QVVEDEDEDEDELTKYGAHVIMLFVPTLCMVVAVATIKSVSYTRKDGLITPTPE 120
QY 121 DTEYGORALHSILNAIMISIVVMTILLVLYKRCYKVIHAWLIISLLFFESFI 180
DB 121 DTEYGORALHSILNAIMISIVVMTILLVLYKRCYKVIHAWLIISLLFFESFI 180
QY 181 YLGEVFKTYNAVDYITVAALLIMNLGVGMISIHMKGPLRLQOAYLIMISALMALVETIKY 240
DB 181 YLGEVFKTYNAVDYITVAALLIMNLGVGMISIHMKGPLRLQOAYLIMISALMALVETIKY 240
QY 241 LPEWTAMILLAVISYDVAVLCPRGRLMLETAEQERNETLFPALITYSTWVWLNNAE 300
DB 241 LPEWTAMILLAVISYDVAVLCPRGRLMLETAEQERNETLFPALITYSTWVWLNNAE 300
QY 301 GDEPQRARVSKSKYNAESTERESQDTVAENDGGFSEEMEQORSHLCPHSTPESRAA 360
DB 301 GDEPQRARVSKSKYNAESTERESQDTVAENDGGFSEEMEQORSHLCPHSTPESRAA 360
QY 361 VOELSSSILAGDEPERGVKGLGDFIFYSVLGKASATASGDMNTTACFAVAILGLCL 420
DB 361 VOELSSSILAGDEPERGVKGLGDFIFYSVLGKASATASGDMNTTACFAVAILGLCL 420
QY 421 TLLLAIFKKALPALPISITFGLVFYPATDYLVOPMDLARHOFYI 467
DB 421 TLLLAIFKKALPALPISITFGLVFYPATDYLVOPMDLARHOFYI 467

RESULT 4

US-09-127-480-2
Sequence 2, Application US/09127480

PATENT NO. 6194153
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,480
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-127-480-2

Query Match 100.0%; Score 2391; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 9,7e-235;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSQSDNHLSTNVRSONDREROENHRRSLGHPPELSNGRPOGNSR 60
DB 1 MTELPAPLSYFQNAQMSQSDNHLSTNVRSONDREROENHRRSLGHPPELSNGRPOGNSR 60
QY 61 QVVEDEDEDEDELTKYGAHVIMLFVPTLCMVVAVATIKSVSYTRKDGLITPTPE 120
DB 61 QVVEDEDEDEDELTKYGAHVIMLFVPTLCMVVAVATIKSVSYTRKDGLITPTPE 120
QY 121 DTEYGORALHSILNAIMISIVVMTILLVLYKRCYKVIHAWLIISLLFFESFI 180
DB 121 DTEYGORALHSILNAIMISIVVMTILLVLYKRCYKVIHAWLIISLLFFESFI 180
QY 181 YLGEVFKTYNAVDYITVAALLIMNLGVGMISIHMKGPLRLQOAYLIMISALMALVETIKY 240
DB 181 YLGEVFKTYNAVDYITVAALLIMNLGVGMISIHMKGPLRLQOAYLIMISALMALVETIKY 240
QY 241 LPEWTAMILLAVISYDVAVLCPRGRLMLETAEQERNETLFPALITYSTWVWLNNAE 300
DB 241 LPEWTAMILLAVISYDVAVLCPRGRLMLETAEQERNETLFPALITYSTWVWLNNAE 300
QY 301 GDEPQRARVSKSKYNAESTERESQDTVAENDGGFSEEMEQORSHLCPHSTPESRAA 360
DB 301 GDEPQRARVSKSKYNAESTERESQDTVAENDGGFSEEMEQORSHLCPHSTPESRAA 360
QY 361 VOELSSSILAGDEPERGVKGLGDFIFYSVLGKASATASGDMNTTACFAVAILGLCL 420
DB 361 VOELSSSILAGDEPERGVKGLGDFIFYSVLGKASATASGDMNTTACFAVAILGLCL 420
QY 421 TLLLAIFKKALPALPISITFGLVFYPATDYLVOPMDLARHOFYI 467
DB 421 TLLLAIFKKALPALPISITFGLVFYPATDYLVOPMDLARHOFYI 467

RESULT 5

US-08-496-841C-2
Sequence 2, Application US/08496841C

PATENT NO. 6210919
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dady & Dady, PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,841C
FILING DATE: 28-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehner, Ph.D.
REGISTRATION NUMBER: 35,135
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-496-841C-2

Query Match 100.0%; Score 2391; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 9.7e-235;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFONAKQSEDNHLSNTVRSQNDNREHNDRRSLGHPPLSNGRPOGNSR 60
1 MTELPAPLSYFONAKQSEDNHLSNTVRSQNDNREHNDRRSLGHPPLSNGRPOGNSR 60
DB 1 MTELPAPLSYFONAKQSEDNHLSNTVRSQNDNREHNDRRSLGHPPLSNGRPOGNSR 60
QY 61 QVVEDEDEDEDELTLYGAKHVMLEFVPYTLQMVVVVATIKVSFTTRDGOLITPPE 120
61 QVVEDEDEDEDELTLYGAKHVMLEFVPYTLQMVVVVATIKVSFTTRDGOLITPPE 120
DB 61 QVVEDEDEDEDELTLYGAKHVMLEFVPYTLQMVVVVATIKVSFTTRDGOLITPPE 120
QY 121 DFTVQGRALHSILNAINISIVVMTLLVLYKRCYKVIHAWLISSLLLEFFSFI 180
121 DFTVQGRALHSILNAINISIVVMTLLVLYKRCYKVIHAWLISSLLLEFFSFI 180
DB 121 DFTVQGRALHSILNAINISIVVMTLLVLYKRCYKVIHAWLISSLLLEFFSFI 180
QY 181 YLGEVFKTYNVAVDYITVALIMNLGVGMISIMHKGPLRLQOAVLIMISALMALVFIRY 240
181 YLGEVFKTYNVAVDYITVALIMNLGVGMISIMHKGPLRLQOAVLIMISALMALVFIRY 240
DB 181 YLGEVFKTYNVAVDYITVALIMNLGVGMISIMHKGPLRLQOAVLIMISALMALVFIRY 240
QY 241 LPEWTAMLILAVISYDVAVLCPRGLRMVETAOERNETLFPALISSTWMLVNNAE 300
241 LPEWTAMLILAVISYDVAVLCPRGLRMVETAOERNETLFPALISSTWMLVNNAE 300
DB 241 LPEWTAMLILAVISYDVAVLCPRGLRMVETAOERNETLFPALISSTWMLVNNAE 300
QY 301 GPEAQRKRSKSKYNAESTERESODTVAENDGGFSEMEQROSHLGPHRSTPESRAA 360
301 GPEAQRKRSKSKYNAESTERESODTVAENDGGFSEMEQROSHLGPHRSTPESRAA 360
DB 301 GPEAQRKRSKSKYNAESTERESODTVAENDGGFSEMEQROSHLGPHRSTPESRAA 360
QY 361 VOELSSSILAGDEPBERGKLGIDFIFYSVLVGKASATASGDMWTTTACFAAILIGLCL 420
361 VOELSSSILAGDEPBERGKLGIDFIFYSVLVGKASATASGDMWTTTACFAAILIGLCL 420
DB 361 VOELSSSILAGDEPBERGKLGIDFIFYSVLVGKASATASGDMWTTTACFAAILIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGIVFEFATDYLVOPFMDLAFHQFYI 467
421 TLLLAIFKKALPALPISITFGIVFEFATDYLVOPFMDLAFHQFYI 467
DB 421 TLLLAIFKKALPALPISITFGIVFEFATDYLVOPFMDLAFHQFYI 467

RESULT 6
US-09-124-523-2
Sequence 2, Application US/09124523
Patent No. 6395960
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: PRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HUMWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street

CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,523
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fletcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-124-523-2

Query Match 100.0%; Score 2391; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 9.7e-235;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFONAKQSEDNHLSNTVRSQNDNREHNDRRSLGHPPLSNGRPOGNSR 60
1 MTELPAPLSYFONAKQSEDNHLSNTVRSQNDNREHNDRRSLGHPPLSNGRPOGNSR 60
DB 1 MTELPAPLSYFONAKQSEDNHLSNTVRSQNDNREHNDRRSLGHPPLSNGRPOGNSR 60
QY 61 QVVEDEDEDEDELTLYGAKHVMLEFVPYTLQMVVVVATIKVSFTTRDGOLITPPE 120
61 QVVEDEDEDEDELTLYGAKHVMLEFVPYTLQMVVVVATIKVSFTTRDGOLITPPE 120
DB 61 QVVEDEDEDEDELTLYGAKHVMLEFVPYTLQMVVVVATIKVSFTTRDGOLITPPE 120
QY 121 DFTVQGRALHSILNAINISIVVMTLLVLYKRCYKVIHAWLISSLLLEFFSFI 180
121 DFTVQGRALHSILNAINISIVVMTLLVLYKRCYKVIHAWLISSLLLEFFSFI 180
DB 121 DFTVQGRALHSILNAINISIVVMTLLVLYKRCYKVIHAWLISSLLLEFFSFI 180
QY 181 YLGEVFKTYNVAVDYITVALIMNLGVGMISIMHKGPLRLQOAVLIMISALMALVFIRY 240
181 YLGEVFKTYNVAVDYITVALIMNLGVGMISIMHKGPLRLQOAVLIMISALMALVFIRY 240
DB 181 YLGEVFKTYNVAVDYITVALIMNLGVGMISIMHKGPLRLQOAVLIMISALMALVFIRY 240
QY 241 LPEWTAMLILAVISYDVAVLCPRGLRMVETAOERNETLFPALISSTWMLVNNAE 300
241 LPEWTAMLILAVISYDVAVLCPRGLRMVETAOERNETLFPALISSTWMLVNNAE 300
DB 241 LPEWTAMLILAVISYDVAVLCPRGLRMVETAOERNETLFPALISSTWMLVNNAE 300
QY 301 GPEAQRKRSKSKYNAESTERESODTVAENDGGFSEMEQROSHLGPHRSTPESRAA 360
301 GPEAQRKRSKSKYNAESTERESODTVAENDGGFSEMEQROSHLGPHRSTPESRAA 360
DB 301 GPEAQRKRSKSKYNAESTERESODTVAENDGGFSEMEQROSHLGPHRSTPESRAA 360
QY 361 VOELSSSILAGDEPBERGKLGIDFIFYSVLVGKASATASGDMWTTTACFAAILIGLCL 420
361 VOELSSSILAGDEPBERGKLGIDFIFYSVLVGKASATASGDMWTTTACFAAILIGLCL 420
DB 361 VOELSSSILAGDEPBERGKLGIDFIFYSVLVGKASATASGDMWTTTACFAAILIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGIVFEFATDYLVOPFMDLAFHQFYI 467
421 TLLLAIFKKALPALPISITFGIVFEFATDYLVOPFMDLAFHQFYI 467
DB 421 TLLLAIFKKALPALPISITFGIVFEFATDYLVOPFMDLAFHQFYI 467

RESULT 7
US-08-967-101-134
Sequence 134, Application US/08967101
Patent No. 5840540
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H

APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-967-101-134

Query Match 99.8%; Score 2387; DB 2; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.5e-234;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNREHNDRLSLGHPPLSNGRQGNR 60
DB 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNREHNDRLSLGHPPLSNGRQGNR 60
QY 61 QVQDEDEDEDELTKYGAHVIMLFVPTLCMVVAVATIKSVSYTRKDGQLYTPETE 120
DB 61 QVQDEDEDEDELTKYGAHVIMLFVPTLCMVVAVATIKSVSYTRKDGQLYTPETE 120
QY 121 DTEYVGAALHSILNAAMISIVYVMTLLVLYKRYKYIHAMLIISSLLLEFFSFI 180
DB 121 DTEYVGAALHSILNAAMISIVYVMTLLVLYKRYKYIHAMLIISSLLLEFFSFI 180
QY 181 YLGEVFKTYNAVDYITVALLIMNGVGMISIHKGPLRLOQAVLIMISALMALVFYKY 240
DB 181 YLGEVFKTYNAVDYITVALLIMNGVGMISIHKGPLRLOQAVLIMISALMALVFYKY 240
QY 241 LPEWTAMILAVISYVDLVAVLCPRKPLMLVETAOERNETLFPALIVSSTWMLVNNAE 300
DB 241 LPEWTAMILAVISYVDLVAVLCPRKPLMLVETAOERNETLFPALIVSSTWMLVNNAE 300
QY 301 GDPENQRRVSKNSKYNASTERSODTYAENDDGFSEEMEQORSHLGPHRSTPESRAA 360
DB 301 GDPENQRRVSKNSKYNASTERSODTYAENDDGFSEEMEQORSHLGPHRSTPESRAA 360
QY 361 VOELSSSLIAGEDPERGVKLGIDFIYSYLVKASATASGDMWTTTACFAVAILIGLCL 420
DB 361 VOELSSSLIAGEDPERGVKLGIDFIYSYLVKASATASGDMWTTTACFAVAILIGLCL 420
QY 421 TLLLLAIKKALPALPISITGVLVYFATDYLVQPFMDQLAFHQFYI 467
DB 421 TLLLLAIKKALPALPISITGVLVYFATDYLVQPFMDQLAFHQFYI 467

RESULT 8
US-08-592-541-134
Sequence 134, Application US/08592541
Patent No. 5986054
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-592-541-134

Query Match 99.8%; Score 2387; DB 2; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.5e-234;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNREHNDRLSLGHPPLSNGRQGNR 60
DB 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNREHNDRLSLGHPPLSNGRQGNR 60
QY 61 QVQDEDEDEDELTKYGAHVIMLFVPTLCMVVAVATIKSVSYTRKDGQLYTPETE 120
DB 61 QVQDEDEDEDELTKYGAHVIMLFVPTLCMVVAVATIKSVSYTRKDGQLYTPETE 120
QY 121 DTEYVGAALHSILNAAMISIVYVMTLLVLYKRYKYIHAMLIISSLLLEFFSFI 180
DB 121 DTEYVGAALHSILNAAMISIVYVMTLLVLYKRYKYIHAMLIISSLLLEFFSFI 180
QY 181 YLGEVFKTYNAVDYITVALLIMNGVGMISIHKGPLRLOQAVLIMISALMALVFYKY 240
DB 181 YLGEVFKTYNAVDYITVALLIMNGVGMISIHKGPLRLOQAVLIMISALMALVFYKY 240
QY 241 LPEWTAMILAVISYVDLVAVLCPRKPLMLVETAOERNETLFPALIVSSTWMLVNNAE 300
DB 241 LPEWTAMILAVISYVDLVAVLCPRKPLMLVETAOERNETLFPALIVSSTWMLVNNAE 300
QY 301 GDPENQRRVSKNSKYNASTERSODTYAENDDGFSEEMEQORSHLGPHRSTPESRAA 360
DB 301 GDPENQRRVSKNSKYNASTERSODTYAENDDGFSEEMEQORSHLGPHRSTPESRAA 360
QY 361 VOELSSSLIAGEDPERGVKLGIDFIYSYLVKASATASGDMWTTTACFAVAILIGLCL 420
DB 361 VOELSSSLIAGEDPERGVKLGIDFIYSYLVKASATASGDMWTTTACFAVAILIGLCL 420

Db 361 VOELSSIIAGEDPERGVKLGIDFIYSVLGKASATASGDMNTTACFVAIIIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGIVFYFANDYLVOPMDLAFHOFYI 467
Db 421 TLLLAIFKKALPALPISITFGIVFYFANDYLVOPMDLAFHOFYI 467
RESULT 9
US-08-923-454A-10
; Sequence 10, Application US/08923454A
; Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Kairan, Eric
APPLICANT: Clinkbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-923-454A-10
Query Match 99.8%; Score 2387; DB 3; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.5e-234;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 121 DRETVGORALHSILNAINAIVSVIIVMTILLVLYKRCYKVIHAWLIISLLLEFFSFI 180
QY 181 YGGEVKTNNVADVTTVALLMNGVGMISIHMKGPRLQOAVYIMISALMAVFIY 240
Db 181 YGGEVKTNNVADVTTVALLMNGVGMISIHMKGPRLQOAVYIMISALMAVFIY 240
QY 241 LPEWTAMLLAVISYVDVAVLCPKGPLRLMVELTAQERNETLEPALLYSTVWVLNMAE 300
Db 241 LPEWTAMLLAVISYVDVAVLCPKGPLRLMVELTAQERNETLEPALLYSTVWVLNMAE 300
QY 301 GPEAQRVSKSKNAESTERESQDTVAENDDGGSEEMEQROSHLCPHSTPESRAA 360
Db 301 GPEAQRVSKSKNAESTERESQDTVAENDDGGSEEMEQROSHLCPHSTPESRAA 360
QY 361 VOELSSIIAGEDPERGVKLGIDFIYSVLGKASATASGDMNTTACFVAIIIGLCL 420
Db 361 VOELSSIIAGEDPERGVKLGIDFIYSVLGKASATASGDMNTTACFVAIIIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGIVFYFANDYLVOPMDLAFHOFYI 467
Db 421 TLLLAIFKKALPALPISITFGIVFYFANDYLVOPMDLAFHOFYI 467
RESULT 10
US-08-670-964-2
; Sequence 2, Application US/08670964
; Patent No. 6010874
GENERAL INFORMATION:
APPLICANT: Hardy, John A.
TITLE OF INVENTION: EARLY ONSET ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road - UM2220; P.O. Box 15
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,964
FILING DATE: 26-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,142
FILING DATE: 13-JUL-1995
APPLICATION NUMBER: 60/001,501
FILING DATE: 18-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: P50358
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-670-964-2
Query Match 99.8%; Score 2387; DB 3; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.5e-234;

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Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTELPAPLSTYFQNMQMSDNHLSMTVRSQNDNREROEHNDRRSLSGHPPLSNGRPOGNSR 60
D 1 MTELPAPLSTYFQNMQMSDNHLSMTVRSQNDNREROEHNDRRSLSGHPPLSNGRPOGNSR 60
QY 61 QVDEDEDEDELTKYGAHVIMLFVPVTLCAVYVATIKSVSYTRKQDQLYTPPTE 120
D 61 QVDEDEDEDELTKYGAHVIMLFVPVTLCAVYVATIKSVSYTRKQDQLYTPPTE 120
QY 121 DTEVVGORALHSILNAIMISIVVMTLLVLYKRYKYIHAMLISSLLFFESFI 180
D 121 DTEVVGORALHSILNAIMISIVVMTLLVLYKRYKYIHAMLISSLLFFESFI 180
QY 181 YLGEVFTYNAVDYITVALLIWMGVGMISIMKGPLRQOAVLIMISALMLVFIKY 240
D 181 YLGEVFTYNAVDYITVALLIWMGVGMISIMKGPLRQOAVLIMISALMLVFIKY 240
QY 241 LPEWTAMLIIVSYDVAVLCRPGPLRMLETVAOERNETLFPALITSSTMVLYNNAE 300
D 241 LPEWTAMLIIVSYDVAVLCRPGPLRMLETVAOERNETLFPALITSSTMVLYNNAE 300
QY 301 GDPAQRVSKNSKYNAESTERESQDVAENDDGFSEMEARQDSHLGPHRSTPESRAA 360
D 301 GDPAQRVSKNSKYNAESTERESQDVAENDDGFSEMEARQDSHLGPHRSTPESRAA 360
QY 361 VOELSSSTILAGEDEPERKVKLGDFIFYSVLVGKASATAGDMNTTACVAILIGLCL 420
D 361 VOELSSSTILAGEDEPERKVKLGDFIFYSVLVGKASATAGDMNTTACVAILIGLCL 420
QY 421 TLLLLATFKKALPALPISITGVLVFEATDYLVOPFMDQLAFHOFYI 467
D 421 TLLLLATFKKALPALPISITGVLVFEATDYLVOPFMDQLAFHOFYI 467

RESULT 11
US-08-888-077A-2
; Sequence 2, Application US/08888077A
; Patent No. 6020143
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR.
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LERNER, DAVID, LITTEMBERG, KRUMHOLZ & MENTLIK
; STREET: 600 SOUTH AVENUE WEST
; CITY: WESTFIELD
; STATE: NJ
; COUNTRY: USA
; ZIP: 07090-1497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: PALISI, THOMAS M
; REGISTRATION NUMBER: 36,629
; REFERENCE/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP CIP IV
; TELEPHONE: (908) 654-5000
; TELEFAX: (908) 654-7866
; INFORMATION FOR SEQ ID NO: 2:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-888-077A-2
Query Match 99.8%; Score 2387; DB 3; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.5e-234;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTELPAPLSTYFQNMQMSDNHLSMTVRSQNDNREROEHNDRRSLSGHPPLSNGRPOGNSR 60
D 1 MTELPAPLSTYFQNMQMSDNHLSMTVRSQNDNREROEHNDRRSLSGHPPLSNGRPOGNSR 60
QY 61 QVDEDEDEDELTKYGAHVIMLFVPVTLCAVYVATIKSVSYTRKQDQLYTPPTE 120
D 61 QVDEDEDEDELTKYGAHVIMLFVPVTLCAVYVATIKSVSYTRKQDQLYTPPTE 120
QY 121 DTEVVGORALHSILNAIMISIVVMTLLVLYKRYKYIHAMLISSLLFFESFI 180
D 121 DTEVVGORALHSILNAIMISIVVMTLLVLYKRYKYIHAMLISSLLFFESFI 180
QY 181 YLGEVFTYNAVDYITVALLIWMGVGMISIMKGPLRQOAVLIMISALMLVFIKY 240
D 181 YLGEVFTYNAVDYITVALLIWMGVGMISIMKGPLRQOAVLIMISALMLVFIKY 240
QY 241 LPEWTAMLIIVSYDVAVLCRPGPLRMLETVAOERNETLFPALITSSTMVLYNNAE 300
D 241 LPEWTAMLIIVSYDVAVLCRPGPLRMLETVAOERNETLFPALITSSTMVLYNNAE 300
QY 301 GDPAQRVSKNSKYNAESTERESQDVAENDDGFSEMEARQDSHLGPHRSTPESRAA 360
D 301 GDPAQRVSKNSKYNAESTERESQDVAENDDGFSEMEARQDSHLGPHRSTPESRAA 360
QY 361 VOELSSSTILAGEDEPERKVKLGDFIFYSVLVGKASATAGDMNTTACVAILIGLCL 420
D 361 VOELSSSTILAGEDEPERKVKLGDFIFYSVLVGKASATAGDMNTTACVAILIGLCL 420
QY 421 TLLLLATFKKALPALPISITGVLVFEATDYLVOPFMDQLAFHOFYI 467
D 421 TLLLLATFKKALPALPISITGVLVFEATDYLVOPFMDQLAFHOFYI 467

RESULT 12
US-09-124-698-134
; Sequence 134, Application US/09124698
; Patent No. 6117978
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/124,698
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/592,541

```

FILED DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-124-698-134

Query Match
Best Local Similarity 99.8%; Score 2387; DB 3; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.5e-234;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSSEDNHLSNTVRSQNDNREROEHNDRLSGHPPLSNGRQGNR 60
DB 1 MTELPAPLSYFQNAQMSSEDNHLSNTVRSQNDNREROEHNDRLSGHPPLSNGRQGNR 60
QY 61 QVEDEDEDEDELTLKYGAKHYIMLFVPTLCMVVVATIKSVSYTRKDGLITPTPE 120
DB 61 QVEDEDEDEDELTLKYGAKHYIMLFVPTLCMVVVATIKSVSYTRKDGLITPTPE 120
QY 121 DTEYQGRALHSILNAAIMISIVYVMTLLVLYRYRCYKVIHAWLIISLLLEFFSFI 180
DB 121 DTEYQGRALHSILNAAIMISIVYVMTLLVLYRYRCYKVIHAWLIISLLLEFFSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLIMNLGVGMISIHMKGPLRLQOAVLIMISALMALVFITY 240
DB 181 YLGEVFKTYNVAVDYITVALLIMNLGVGMISIHMKGPLRLQOAVLIMISALMALVFITY 240
QY 241 LPEWTAAILAVISYDVAVLCPRGLMLVETAQERNETLFPALIVYSTWVWLNNAE 300
DB 241 LPEWTAAILAVISYDVAVLCPRGLMLVETAQERNETLFPALIVYSTWVWLNNAE 300
QY 301 GPEAQRYSKSKYNAESTERESODTYAENDDGFSEMEQORSHLGPFRSTPESRAA 360
DB 301 GPEAQRYSKSKYNAESTERESODTYAENDDGFSEMEQORSHLGPFRSTPESRAA 360
QY 361 VOELSSSILAGDEPERGVKLGDFIFYSVLVGKASATASGDWMTTACFAVAILIGLCL 420
DB 361 VOELSSSILAGDEPERGVKLGDFIFYSVLVGKASATASGDWMTTACFAVAILIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGLVFPATDYLVQPFMDQLAHHQFYI 467
DB 421 TLLLAIFKKALPALPISITFGLVFPATDYLVQPFMDQLAHHQFYI 467

RESULT 13
US-09-127-480-134
Sequence 134, Application US/09127480
Patent No. 6194153
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESS: TESTA, HUMWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,480
FILED DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILED DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-127-480-134

Query Match
Best Local Similarity 99.8%; Score 2387; DB 4; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.5e-234;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSSEDNHLSNTVRSQNDNREROEHNDRLSGHPPLSNGRQGNR 60
DB 1 MTELPAPLSYFQNAQMSSEDNHLSNTVRSQNDNREROEHNDRLSGHPPLSNGRQGNR 60
QY 61 QVEDEDEDEDELTLKYGAKHYIMLFVPTLCMVVVATIKSVSYTRKDGLITPTPE 120
DB 61 QVEDEDEDEDELTLKYGAKHYIMLFVPTLCMVVVATIKSVSYTRKDGLITPTPE 120
QY 121 DTEYQGRALHSILNAAIMISIVYVMTLLVLYRYRCYKVIHAWLIISLLLEFFSFI 180
DB 121 DTEYQGRALHSILNAAIMISIVYVMTLLVLYRYRCYKVIHAWLIISLLLEFFSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLIMNLGVGMISIHMKGPLRLQOAVLIMISALMALVFITY 240
DB 181 YLGEVFKTYNVAVDYITVALLIMNLGVGMISIHMKGPLRLQOAVLIMISALMALVFITY 240
QY 241 LPEWTAAILAVISYDVAVLCPRGLMLVETAQERNETLFPALIVYSTWVWLNNAE 300
DB 241 LPEWTAAILAVISYDVAVLCPRGLMLVETAQERNETLFPALIVYSTWVWLNNAE 300
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QY 361 VOELSSSILAGDEPERGVKLGDFIFYSVLVGKASATASGDWMTTACFAVAILIGLCL 420
DB 361 VOELSSSILAGDEPERGVKLGDFIFYSVLVGKASATASGDWMTTACFAVAILIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGLVFPATDYLVQPFMDQLAHHQFYI 467
DB 421 TLLLAIFKKALPALPISITFGLVFPATDYLVQPFMDQLAHHQFYI 467

RESULT 14
US-08-496-841C-134
Sequence 134, Application US/08496841C
Patent No. 6210919
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESS: Darby & Darby, PC

STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,841C
FILING DATE: 28-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehlner, Ph.D.
REGISTRATION NUMBER: 35,135
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ. ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 134:
US-08-496-841C-134

Query Match 99.8%; Score 2387; DB 4; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.5e-234;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 241 LPEWTAMLLAVISYVDLVAVLCPRGRLMLETAEQERNETLFPALIVSSTWMLVNNAE 300
QY 301 GDPEAQRVSKNSKYNAESTERESODTYAENDDGFSEMEQAQRDHLGPHRSTPESRAA 360
DB 301 GDPEAQRVSKNSKYNAESTERESODTYAENDDGFSEMEQAQRDHLGPHRSTPESRAA 360
QY 361 VOELSSSTILAGEDPEERGVKLGDFIFYSVLVGKASATASGDMNTTACFAVAILIGLCL 420
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QY 421 TLLLAIFKKALPALPISITFGLVFYFATDYLVOFPMQDLAFHOFYI 467
DB 421 TLLLAIFKKALPALPISITFGLVFYFATDYLVOFPMQDLAFHOFYI 467

RESULT 15
US-08-832-867-3
Sequence 3, Application US/08832867C
Patent No. 6376239
GENERAL INFORMATION:
APPLICANT: BAUMEISTER, Ralf

TITLE OF INVENTION: DNA MOLECULES COMPRISING A PROMOTER CAPABLE OF
TITLE OF INVENTION: CONFERRING EXPRESSION OF A HETEROLOGOUS DNA SEQUENCE IN
TITLE OF INVENTION: ALL NEURAL CELLS AT ALL STAGES OF DEVELOPMENT IN C.
FILE REFERENCE: 674503-2004
CURRENT APPLICATION NUMBER: US/08/832,867C
CURRENT FILING DATE: 1997-04-04
NUMBER OF SEQ. ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 467
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-08-832-867-3

Query Match 99.8%; Score 2387; DB 4; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.5e-234;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 241 LPEWTAMLLAVISYVDLVAVLCPRGRLMLETAEQERNETLFPALIVSSTWMLVNNAE 300
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DB 301 GDPEAQRVSKNSKYNAESTERESODTYAENDDGFSEMEQAQRDHLGPHRSTPESRAA 360
QY 361 VOELSSSTILAGEDPEERGVKLGDFIFYSVLVGKASATASGDMNTTACFAVAILIGLCL 420
DB 361 VOELSSSTILAGEDPEERGVKLGDFIFYSVLVGKASATASGDMNTTACFAVAILIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGLVFYFATDYLVOFPMQDLAFHOFYI 467
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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 20:10:01 ; Search time 17 Seconds
(Without alignments)
1266.176 Million cell updates/sec

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Perfect score: 2391
Sequence: 1 MTELPAPLSTYFQNAQMSQDN.....ATDYLVPFMDQLAFHQFYI 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*

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- 2: /cgn2_6/ptodata/2/pubppa/PCRT_NEW_PUB.pep:*
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- 10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2387	99.8	467	10	US-09-878-454A-3
3	2387	99.8	467	10	US-09-895-035-14
4	2387	99.8	467	12	US-10-071-900-1
5	2382	99.6	467	10	US-09-785-474-2
6	2377	99.4	467	10	US-09-785-474-32
7	2372	99.2	467	10	US-09-785-474-30
8	2370	99.1	467	10	US-09-785-474-28
9	2357	98.6	463	10	US-09-885-035-12
10	2355	98.5	467	10	US-09-785-474-4
11	1461	61.1	448	10	US-09-878-454A-1
12	1461	61.1	448	12	US-10-071-900-2
13	1453	60.8	448	10	US-09-754-949-6
14	798.5	33.4	354	10	US-09-895-035-1
15	658.5	27.6	354	10	US-09-823-153-8
16	380	15.9	101	9	US-09-925-299-1227
17	376.5	15.7	131	9	US-09-925-299-1227
18	376.5	15.7	131	9	US-10-051-767-10
19	366.5	15.3	129	9	US-10-051-767-11

20	344	14.4	210	9	US-10-051-767-12	Sequence 12, Appl
21	308	12.9	166	9	US-10-051-767-7	Sequence 7, Appl
22	308	12.9	166	9	US-10-051-767-13	Sequence 13, Appl
23	256	10.7	74	9	US-10-051-767-9	Sequence 9, Appl
24	256	10.7	74	9	US-10-051-767-15	Sequence 15, Appl
25	243.5	10.2	65	10	US-09-864-761-38056	Sequence 38056, A
26	206	8.6	124	9	US-10-051-767-8	Sequence 8, Appl
27	206	8.6	124	9	US-10-051-767-14	Sequence 14, Appl
28	120.5	5.0	665	10	US-09-942-447-2	Sequence 2, Appl
29	112	4.7	601	10	US-09-884-430-8	Sequence 8, Appl
30	110	4.6	601	10	US-09-782-980-84	Sequence 84, Appl
31	108	4.5	406	9	US-09-966-782A-2	Sequence 2, Appl
32	108	4.5	406	9	US-09-828-432-3	Sequence 3, Appl
33	108	4.5	419	10	US-09-766-693-2	Sequence 2, Appl
34	108	4.5	419	10	US-09-828-432-2	Sequence 2, Appl
35	108	4.5	461	9	US-10-080-960-5	Sequence 5, Appl
36	107	4.5	831	10	US-09-789-561-86	Sequence 86, Appl
37	101.5	4.2	801	9	US-09-738-626-3760	Sequence 3760, Ap
38	99	4.1	730	9	US-09-738-626-4196	Sequence 4196, Ap
39	97	4.1	383	9	US-09-738-626-5701	Sequence 5701, Ap
40	97	4.1	764	9	US-10-045-624B-2	Sequence 2, Appl
41	97	4.1	877	10	US-09-815-242-4901	Sequence 4901, Ap
42	97	4.1	880	10	US-09-815-242-10491	Sequence 10491, A
43	94.5	4.0	737	9	US-09-899-482-2	Sequence 2, Appl
44	94	3.9	2092	9	US-10-147-026-12	Sequence 12, Appl
45	93.5	3.9	850	10	US-09-985-675-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1									
US-09-754-949-4									
: Sequence 4, Application US/09754949									
: Patent No. US20020015939A1									
: GENERAL INFORMATION:									
: APPLICANT: MCCARTHY, JUSTIN									
: APPLICANT: CORDELL, BARBARA									
: TITLE OF INVENTION: METHODS FOR IDENTIFYING INHIBITORS OF									
: FILE REFERENCE: SCIOS.012A									
: CURRENT APPLICATION NUMBER: US/09/754.949									
: CURRENT FILING DATE: 2001-01-04.									
: NUMBER OF SEQ ID NOS: 16									
: SOFTWARE: FastSeq for Windows Version 4.0									
: SEQ ID NO 4									
: LENGTH: 467									
: TYPE: PRT									
: ORGANISM: Homo Sapien									
US-09-754-949-4									
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Best Local Similarity 99.8%; Score 2387; DB 10; Length 467;									
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
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DB	61	QVVEDDEDEDELTKYGAHVIMLFVPTLCMVVVAVATKVSFTRDGLITTPFTE	120						
QY	121	DTEVGORALSHLSNAAMISIVVMTLLVLYKRCYVIAHMLISSLLFFFSFI	180						
DB	121	DTEVGORALSHLSNAAMISIVVMTLLVLYKRCYVIAHMLISSLLFFFSFI	180						
QY	181	YIGEVFKYINAVDVITVALLIMNIGVGMISIMHKGPLRDOAVLIMSALMAVFTKY	240						
DB	181	YIGEVFKYINAVDVITVALLIMNIGVGMISIMHKGPLRDOAVLIMSALMAVFTKY	240						
QY	241	IPENYAMLILAVISYVDLVAVCPKGPLMLVETQERETLPALISSTVWVIVNNAE	300						
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Db 241 LPEWTAMLLIAYISYDVAVLCPKPLRMVETFAOERNETLEPALIYSTWMLVNNMAE 300
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Db 301 GDEAORRVSKSKNYAESTERESODTVAENDDGGFSEMEAO RDSHLGPHRSTPESRAA 360
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Db 361 VOELSSSIAGDEPBERGVKLGIDFIYFVSVLVGKASATASGDMNTTACFAVAILIGLCL 420
Qy 421 TLLLLAIFKKALPALPISITFGVLFYFADYLVOPMDLAFHOEYI 467
Db 421 TLLLLAIFKKALPALPISITFGVLFYFADYLVOPMDLAFHOEYI 467

RESULT 2
US-09-878-454A-3
; Sequence 3, Application US/09878454A
; Patent No. US20020064828A1
; GENERAL INFORMATION:
; APPLICANT: Monteliro, et al.
; TITLE OF INVENTION: Method of controlling the binding of Calmyrin to Presenilin
; FILE REFERENCE: 4115-161
; CURRENT APPLICATION NUMBER: US/09/878,454A
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/210,939
; PRIOR FILING DATE: 2000-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-878-454A-3

Query Match 99.8%; Score 2387; DB 10; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.7e-207;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 361 VOELSSSIAGDEPBERGVKLGIDFIYFVSVLVGKASATASGDMNTTACFAVAILIGLCL 420
Qy 421 TLLLLAIFKKALPALPISITFGVLFYFADYLVOPMDLAFHOEYI 467
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RESULT 3
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US-09-895-035-14
; Sequence 14, Application US/09895035
; Patent No. US20020082211A1
; GENERAL INFORMATION:
; APPLICANT: Patterson, Chandra
; APPLICANT: Murry, Lynn E.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PRESENILIN VARIANT
; FILE REFERENCE: PC-0047 CIP
; CURRENT APPLICATION NUMBER: US/09/895,035
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/116,640
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PERL Program
; SEQ ID NO 14
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020082211A1 g1709856
US-09-895-035-14

Query Match 99.8%; Score 2387; DB 10; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.7e-207;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 61 QVVEDEDEDEDELTLYGAKHVIIMLFVPTLCMVVVAVATIKSVFTRKDGOLITPTPE 120
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RESULT 4
US-10-071-900-1
; Sequence 1, Application US/10071900
; Patent No. US20020127541A1
; GENERAL INFORMATION:
; APPLICANT: St. George-Hyslop, Peter H.
; APPLICANT: Rommens, Johanna
; APPLICANT: Fraser, Paul E.
; TITLE OF INVENTION: Alzheimer's Related Proteins and Methods
; FILE REFERENCE: of Use
; CURRENT APPLICATION NUMBER: US/10/071,900
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;; CURRENT FILING DATE: 2002-02-08
;; PRIOR APPLICATION NUMBER: US/09/227,725
;; PRIOR FILING DATE: 1999-01-08
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 1
;; LENGTH: 467
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-071-900-1

Query Match 99.8%; Score 2387; DB 12; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.7e-207;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 361 VOELSSSILAGDPREGVKLGIDGFIYSYLVGKASATASGDWNTTACFAAILGLCL 420
QY 421 TLLLAIFKKALPALPISITFGLVFFATDYVOPMDLAFHOFYI 467
DB 421 TLLLAIFKKALPALPISITFGLVFFATDYVOPMDLAFHOFYI 467

RESULT 5

US-09-785-474-2
; Sequence 2, Application US/09785474
; Patent No. US20010012626A1
; GENERAL INFORMATION:
; APPLICANT: TANZI, RUDOLPH
; MASCO, WILMA
; TITLE OF INVENTION: Genetic Alterations Related To Familial
; Alzheimer's Disease
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/785,474
; FILING DATE: 20-Feb-2001

;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/706,344
;; FILING DATE: 30-AUG-1996
;; APPLICATION NUMBER: 60/003,054
;; FILING DATE: 31-AUG-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: KIM, JUDITH U.
;; REGISTRATION NUMBER: 40,679
;; REFERENCE/DOCKET NUMBER: 0609.4180002
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 467 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-785-474-2

Query Match 99.6%; Score 2382; DB 10; Length 467;
Best Local Similarity 99.6%; Pred. No. 7.6e-207;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAFLSYFQNAQSEDNHLSNTVRSONDRERHNDRLSLGHPPLSGRPGNSR 60
DB 1 MTELPAFLSYFQNAQSEDNHLSNTVRSONDRERHNDRLSLGHPPLSGRPGNSR 60
QY 61 QVVEDDEDEDELTKYGAKHVIMLFVPTLCMVVVAATIKSVSYTRKDGOLITPTPE 120
DB 61 QVVEDDEDEDELTKYGAKHVIMLFVPTLCMVVVAATIKSVSYTRKDGOLITPTPE 120
QY 121 DTEVGOALHSILNAAMISVIYVMTILVLYKRCYKVIHAWLIISLLLEFFSFI 180
DB 121 DTEVGOALHSILNAAMISVIYVMTILVLYKRCYKVIHAWLIISLLLEFFSFI 180
QY 181 YLGEVFKYNNVADVITYALLIMNCGVGMISIHMKGPLRLOQAVLIMSALMALVFIKY 240
DB 181 YLGEVFKYNNVADVITYALLIMNCGVGMISIHMKGPLRLOQAVLIMSALMALVFIKY 240
QY 241 LPEMTAMLLAVISYVDLAVLCPKGPLMLVETAQERNETLFPALITYSTWMLVNMME 300
DB 241 LPEMTAMLLAVISYVDLAVLCPKGPLMLVETAQERNETLFPALITYSTWMLVNMME 300
QY 301 GQPEAQRVSKSKYNAESTERESQDTVAENDDGFSEEMEAQRDRLGPHRSTPESRAA 360
DB 301 GQPEAQRVSKSKYNAESTERESQDTVAENDDGFSEEMEAQRDRLGPHRSTPESRAA 360
QY 361 VOELSSSILAGDPREGVKLGIDGFIYSYLVGKASATASGDWNTTACFAAILGLCL 420
DB 361 VOELSSSILAGDPREGVKLGIDGFIYSYLVGKASATASGDWNTTACFAAILGLCL 420
QY 421 TLLLAIFKKALPALPISITFGLVFFATDYVOPMDLAFHOFYI 467
DB 421 TLLLAIFKKALPALPISITFGLVFFATDYVOPMDLAFHOFYI 467

RESULT 6

US-09-785-474-32
; Sequence 32, Application US/09785474
; Patent No. US20010012626A1
; GENERAL INFORMATION:
; APPLICANT: TANZI, RUDOLPH
; MASCO, WILMA
; TITLE OF INVENTION: Genetic Alterations Related To Familial
; Alzheimer's Disease
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON

STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/785,474
FILING DATE: 20-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/706,344
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609.4180002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-785-474-32

Query Match 99.4%; Score 2377; DB 10; Length 467;
Best Local Similarity 99.4%; Pred. No. 2,1e-206;
Matches 464; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTELPAPLSTFQNAQMSSEDNHLSNTVRSQNDNREORHNDRLSLGHPPLSNGRPGNSR 60
DB 1 MTELPAPLSTFQNAQMSSEDNHLSNTVRSQNDNREORHNDRLSLGHPPLSNGRPGNSR 60
QY 61 QVVEODEEEDDELTKYGAHVIMLFVPTLCVWVAVATIKSVFTRKDGQILYPTFE 120
DB 61 QVVEODEEEDDELTKYGAHVIMLFVPTLCVWVAVATIKSVFTRKDGQILYPTFE 120
QY 121 DFTVGOALHSILNAIMISVIVMTILLVLYKRCYKVIHAWLIISSLLFFFSFI 180
DB 121 DFTVGOALHSILNAIMISVIVMTILLVLYKRCYKVIHAWLIISSLLFFFSFI 180
QY 181 YLGEVEKTYNAVDYITVALLINLGVNGISIHMKGPLRLQOAYLIMISALMALVFIKY 240
DB 181 YLGEVEKTYNAVDYITVALLINLGVNGISIHMKGPLRLQOAYLIMISALMALVFIKY 240
QY 241 LPFWTAMLLAVISYDVAVLCPRKPLRMVETAOERNETLFPALYSTWMLVNMME 300
DB 241 LPFWTAMLLAVISYDVAVLCPRKPLRMVETAOERNETLFPALYSTWMLVNMME 300
QY 301 GDEPAORRVSKNSKNAESTERESODTVAENDDGGFSEMEARQDSHLGPHRSTPESRAA 360
DB 301 GDEPAORRVSKNSKNAESTERESODTVAENDDGGFSEMEARQDSHLGPHRSTPESRAA 360
QY 361 VOELSSSILAGDEPBERGVKLGDFIFYSVLVGKASATASGDMNTTIACFAAILIGLCL 420
DB 361 VOELSSSILAGDEPBERGVKLGDFIFYSVLVGKASATASGDMNTTIACFAAILIGLCL 420
QY 421 TLLLLAIFKKALPALPISITFGLVFFATDYLVQPFMDLAHFQFI 467
DB 421 TLLLLAIFKKALPALPISITFGLVFFATDYLVQPFMDLAHFQFI 467

RESULT 7
US-09-785-474-30
Sequence 30, Application US/09785474

Patent No. US20010012626A1
GENERAL INFORMATION:
APPLICANT: TANZI, RUDOLPH
MASCO, WILMA
TITLE OF INVENTION: Genetic Alterations Related To Familial
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/785,474
FILING DATE: 20-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/706,344
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609.4180002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-785-474-30

Query Match 99.2%; Score 2372; DB 10; Length 467;
Best Local Similarity 99.4%; Pred. No. 6e-206;
Matches 464; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTELPAPLSTFQNAQMSSEDNHLSNTVRSQNDNREORHNDRLSLGHPPLSNGRPGNSR 60
DB 1 MTELPAPLSTFQNAQMSSEDNHLSNTVRSQNDNREORHNDRLSLGHPPLSNGRPGNSR 60
QY 61 QVVEODEEEDDELTKYGAHVIMLFVPTLCVWVAVATIKSVFTRKDGQILYPTFE 120
DB 61 QVVEODEEEDDELTKYGAHVIMLFVPTLCVWVAVATIKSVFTRKDGQILYPTFE 120
QY 121 DFTVGOALHSILNAIMISVIVMTILLVLYKRCYKVIHAWLIISSLLFFFSFI 180
DB 121 DFTVGOALHSILNAIMISVIVMTILLVLYKRCYKVIHAWLIISSLLFFFSFI 180
QY 181 YLGEVEKTYNAVDYITVALLINLGVNGISIHMKGPLRLQOAYLIMISALMALVFIKY 240
DB 181 YLGEVEKTYNAVDYITVALLINLGVNGISIHMKGPLRLQOAYLIMISALMALVFIKY 240
QY 241 LPFWTAMLLAVISYDVAVLCPRKPLRMVETAOERNETLFPALYSTWMLVNMME 300
DB 241 LPFWTAMLLAVISYDVAVLCPRKPLRMVETAOERNETLFPALYSTWMLVNMME 300
QY 301 GDEPAORRVSKNSKNAESTERESODTVAENDDGGFSEMEARQDSHLGPHRSTPESRAA 360
DB 301 GDEPAORRVSKNSKNAESTERESODTVAENDDGGFSEMEARQDSHLGPHRSTPESRAA 360
QY 361 VOELSSSILAGDEPBERGVKLGDFIFYSVLVGKASATASGDMNTTIACFAAILIGLCL 420

|||||
Db 361 VOELSSSTLAGEDEBERGVKLGDFIFYSVLVGKASATASGDMNTTACFVAILIGLCL 420
Qy 421 TLLLATIFKKALPALPISITFGVLFYFATDVLVOPFMDQLAFHOFYI 467
|||||
Db 421 TLLLATIFKKALPALPISITFGVLFYFATDVLVOPFMDQLAFHOFYI 467

RESULT 8
US-09-785-474-28

; Sequence 28, Application US/09785474
; Patent No. US20010012626a1
; GENERAL INFORMATION:
; APPLICANT: TANZI, RUDOLPH
; MASCO, WILLMA
; TITLE OF INVENTION: Genetic Alterations Related To Familial
; Alzheimer's Disease
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION NUMBER: US/09/785,474
; APPLICATION NUMBER: US/09/785,474
; FILING DATE: 20-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIORITY DATA:
; APPLICATION NUMBER: 08/706,344
; FILING DATE: 30-AUG-1996
; APPLICATION NUMBER: 60/003,054
; FILING DATE: 31-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KIM, JUDITH U.
; REGISTRATION NUMBER: 40,679
; REFERENCE/DOCKET NUMBER: 0609,4180002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-785-474-28

Query Match 99.1%; Score 2370; DB 10; Length 467;
Best Local Similarity 99.4%; Pred. No. 9,1e-206;
Matches 46; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MTELPAPLSTYFQNMOMSEDNHLSTNVRSONDREROEHNDRRSLGHPPLSNGRPOGNSR 60
|||||
Db 1 MTELPAPLSTYFQNMOMSEDNHLSTNVRSONDREROEHNDRRSLGHPPLSNGRPOGNSR 60
|||||
Qy 61 QVVEQDEDEDELTKYGAKHIVMLFVPTLCMVVVVATIKSVSFYTRKDGQLIYTPTE 120
|||||
Db 61 QVVEQDEDEDELTKYGAKHIVMLFVPTLCMVVVVATIKSVSFYTRKDGQLIYTPTE 120
|||||
Qy 121 DTEVVGORALSHINAAIMISIVVMTLLVLYKRCYKVIHAMLIISSLLFFPSFI 180
|||||
Db 121 DTEVVGORALSHINAAIMISIVVMTLLVLYKRCYKVIHAMLIISSLLFFPSFI 180
|||||
Qy 181 YLGEVFTYVNAVDTYVALLIIMNGVVGMSIHMKGPLRLQOAYLIMISALMLVFIKY 240
|||||

Db 181 YLGEVFTYVNAVDTYVALLIIMNGVVGMSIHMKGPLRLQOAYLIMISALMLVFIKY 240
Qy 241 LPEWTAMLLIAVISVYDVAALCPKGPLRMLVETAOERNETLPALIISSMTWMLVNNAE 300
|||||
Db 241 LPEWTAMLLIAVISVYDVAALCPKGPLRMLVETAOERNETLPALIISSMTWMLVNNAE 300
|||||
Qy 301 GDPAQRVSKNSKYNMESTERESODTYAENDDGFSEMEAOQSDSHGPRHSTPESRAA 360
|||||
Db 301 GDPAQRVSKNSKYNMESTERESODTYAENDDGFSEMEAOQSDSHGPRHSTPESRAA 360
|||||
Qy 361 VOELSSSTLAGEDEBERGVKLGDFIFYSVLVGKASATASGDMNTTACFVAILIGLCL 420
|||||
Db 361 VOELSSSTLAGEDEBERGVKLGDFIFYSVLVGKASATASGDMNTTACFVAILIGLCL 420
|||||
Qy 421 TLLLATIFKKALPALPISITFGVLFYFATDVLVOPFMDQLAFHOFYI 467
|||||
Db 421 TLLLATIFKKALPALPISITFGVLFYFATDVLVOPFMDQLAFHOFYI 467
|||||

RESULT 9
US-09-895-035-12

; Sequence 12, Application US/09895035
; Patent No. US20020082211A1
; GENERAL INFORMATION:
; APPLICANT: Patterson, Chandra
; APPLICANT: Murry, Lynn E.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PRESENILIN VARIANT
; FILE REFERENCE: PC-0047 CIP
; CURRENT APPLICATION NUMBER: US/09/895,035
; CURRENT FILING DATE: 2001-06-29
; PRIORITY APPLICATION NUMBER: 09/116,640
; PRIORITY FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No. US20020082211A1 g1244638
US-09-895-035-12

Query Match 98.6%; Score 2357; DB 10; Length 463;
Best Local Similarity 98.9%; Pred. No. 1,3e-204;
Matches 46; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

Qy 1 MTELPAPLSTYFQNMOMSEDNHLSTNVRSONDREROEHNDRRSLGHPPLSNGRPOGNSR 60
|||||
Db 1 MTELPAPLSTYFQNMOMSEDNHLSTNVRSONDREROEHNDRRSLGHPPLSNGRPOGNSR 60
|||||
Qy 61 QVVEQDEDEDELTKYGAKHIVMLFVPTLCMVVVVATIKSVSFYTRKDGQLIYTPTE 120
|||||
Db 57 QVVEQDEDEDELTKYGAKHIVMLFVPTLCMVVVVATIKSVSFYTRKDGQLIYTPTE 116
|||||
Qy 121 DTEVVGORALSHINAAIMISIVVMTLLVLYKRCYKVIHAMLIISSLLFFPSFI 180
|||||
Db 117 DTEVVGORALSHINAAIMISIVVMTLLVLYKRCYKVIHAMLIISSLLFFPSFI 176
|||||
Qy 181 YLGEVFTYVNAVDTYVALLIIMNGVVGMSIHMKGPLRLQOAYLIMISALMLVFIKY 240
|||||
Db 177 YLGEVFTYVNAVDTYVALLIIMNGVVGMSIHMKGPLRLQOAYLIMISALMLVFIKY 236
|||||
Qy 241 LPEWTAMLLIAVISVYDVAALCPKGPLRMLVETAOERNETLPALIISSMTWMLVNNAE 300
|||||
Db 237 LPEWTAMLLIAVISVYDVAALCPKGPLRMLVETAOERNETLPALIISSMTWMLVNNAE 296
|||||
Qy 301 GDPAQRVSKNSKYNMESTERESODTYAENDDGFSEMEAOQSDSHGPRHSTPESRAA 360
|||||
Db 297 GDPAQRVSKNSKYNMESTERESODTYAENDDGFSEMEAOQSDSHGPRHSTPESRAA 356
|||||
Qy 361 VOELSSSTLAGEDEBERGVKLGDFIFYSVLVGKASATASGDMNTTACFVAILIGLCL 420
|||||

DB 357 VOELSSSILAGDEPERGVKLGDFIFYSVLGKASATASGDMWNTTACFAVAILIGLCL 416
QY 421 TLLLAIFKKALPALPISITFGVLFYFATDYLQPFMDLAFHOFYI 467
DB 417 TLLLAIFKKALPALPISITFGVLFYFATDYLQPFMDLAFHOFYI 463

RESULT 10
US-09-785-474-4
Sequence 4, Application US/09785474
Patent No. US20010012626A1
GENERAL INFORMATION:
APPLICANT: TANZI, RUDOLPH
MASCO, WILMA
TITLE OF INVENTION: Genetic Alterations Related To Familial
Alzheimer's Disease
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/09/785,474
APPLICATION NUMBER: US/09/785,474
FILING DATE: 20-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/706,344
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609,4180002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-785-474-4

Query Match 98.5%; Score 2355; DB 10; Length 467;
Best Local Similarity 98.9%; Pred. No. 2,1e-204;
Matches 462; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MELPAPLSTFQNAQMSDNHLSNTVRSQNDNRERQEHNDRLSLGHPEPLSNRGROGNSR 60
DB 1 MELPAPLSTFQNAQMSDNHLSNTVRSQNDNRERQEHNDRLSLGHPEPLSNRGROGNSR 60
QY 61 QVVEDEDEDELTLYGAKHVIMLFVPTLCMVVVVATIKVSFYTRKDGOLITPTFE 120
DB 61 QVVEDEDEDELTLYGAKHVIMLFVPTLCMVVVVATIKVSFYTRKDGOLITPTFE 120
QY 121 DRETVGQALHSILNAIMISIVVMTLLVLYKYRCYVIAHMLISSLLEFFESFI 180
DB 121 DRETVGQALHSILNAIMISIVVMTLLVLYKYRCYVIAHMLISSLLEFFESFI 180
QY 181 YGGEVFKTYNNAVDTYVALLIWNIGVGMISIHMKGPLRLQOAVLIMISALMALVFYIKY 240

DB 181 YGGEVFKTYNNAVDTYVALLIWNIGVGMISIHMKGPLRLQOAVLIMISALMALVFYIKY 240
QY 241 LPEWTAMILLAVISYVDLVAVLCPKGPLMLVETAQERNETLFPALLIYSTWVLVNNAE 300
DB 241 LPEWTAMILLAVISYVDLVAVLCPKGPLMLVETAQERNETLFPALLIYSTWVLVNNAE 300
QY 301 GDEAQRVSKNSKYNASTEREESODTVAENDDGGFSEEMEAQRDSHLCPHSTPESRAA 360
DB 301 GDEAQRVSKNSKYNASTEREESODTVAENDDGGFSEEMEAQRDSHLCPHSTPESRAA 360
QY 361 VOELSSSILAGDEPERGVKLGDFIFYSVLGKASATASGDMWNTTACFAVAILIGLCL 420
DB 361 VOELSSSILAGDEPERGVKLGDFIFYSVLGKASATASGDMWNTTACFAVAILIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGVLFYFATDYLQPFMDLAFHOFYI 467
DB 421 TLLLAIFKKALPALPISITFGVLFYFATDYLQPFMDLAFHOFYI 467

RESULT 11
US-09-878-454A-1
Sequence 1, Application US/09878454A
Patent No. US20020064828A1
GENERAL INFORMATION:
APPLICANT: Monteliro, et al.
TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presentin
FILE REFERENCE: 4115-161
CURRENT APPLICATION NUMBER: US/09/878,454A
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/210,939
PRIOR FILING DATE: 2000-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 448
TYPE: PRT
ORGANISM: Homo sapiens
US-09-878-454A-1

Query Match 61.1%; Score 1461; DB 10; Length 448;
Best Local Similarity 65.5%; Pred. No. 8.7e-124;
Matches 305; Conservative 39; Mismatches 80; Indels 42; Gaps 8;

QY 3 ELAPLSTFQNAQMSDNHLSNTVRSQNDNRERQEHNDRLSLGHPEPLSNRGROGNSRQ 61
DB 24 ESPTRSCQEGRGDEGENTAQMSQNEDEEDDPDYCVSVP-----GRPG---- 74
QY 62 VVEQDEDEDELTLYGAKHVIMLFVPTLCMVVVVATIKVSFYTRKDGOLITPTFE 121
DB 75 -----LEELTLKYGAKHVIMLFVPTLCMIVVAVATIKVSFYTRKDGOLITPTFE 127
QY 122 TETVGQALHSILNAIMISIVVMTLLVLYKYRCYVIAHMLISSLLEFFESFI 181
DB 128 TPVGQRLNSVNLIMISIVVMTLLVLYKYRCYVIAHMLISSLLEFFESFI 187
QY 182 IGEVFKTYNNAVDTYVALLIWNIGVGMISIHMKGPLRLQOAVLIMISALMALVFYIKYL 241
DB 188 IGEVFKTYNNAVDTYVALLIWNIGVGMISIHMKGPLRLQOAVLIMISALMALVFYIKYL 247
QY 242 PWTAMILLAVISYVDLVAVLCPKGPLMLVETAQERNETLFPALLIYSTWVLVNNAE 301
DB 248 PWTAMILLAVISYVDLVAVLCPKGPLMLVETAQERNETLFPALLIYSTWVLVNNAE 307
QY 302 DEEAQRVSKNSKYNASTEREESODTVAENDDGGFSEEMEAQRDSHLCPHSTPESRAA 361
DB 308 DPSSQAL--QLPYPE--MEEDSYSGE--PSTPEVPEPLTGYG----- 349
QY 362 QELSSSILAGDEPERGVKLGDFIFYSVLGKASATASGDMWNTTACFAVAILIGLCL 421
DB 350 BEL-----EEEBRGVYLGIDFIFYSVLGKAAATGSGDMWNTTACFAVAILIGLCL 402
QY 422 TLLLAIFKKALPALPISITFGVLFYFATDYLQPFMDLAFHOFYI 467

Db 403 LLLAVFKKALPALPISITFGILIFYSTDNLVPRPMDTLASHOLYI 448

RESULT 12

US-10-071-900-2

Sequence 2, Application US/10071900

Patent No. US2002012751A1

GENERAL INFORMATION:

APPLICANT: St. George-Hyslop, Peter H.

APPLICANT: Rommens, Johanna

APPLICANT: Fraser, Paul E.

TITLE OF INVENTION: Alzheimer's Related Proteins and Methods

TITLE OF INVENTION: of Use

FILE REFERENCE: 1034/1F810-US1

CURRENT APPLICATION NUMBER: US/10/071,900

PRIOR FILING DATE: 2002-02-08

PRIOR APPLICATION NUMBER: US/09/227,725

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 448

TYPE: PRT

ORGANISM: Homo Sapien

US-10-071-900-2

Query Match 61.1%; Score 1461; DB 12; Length 448;

Best Local Similarity 65.5%; Pred. No. 8.7e-124;

Matches 305; Conservative 39; Mismatches 80; Indels 42; Gaps 8;

QY 3 ELPAALSYFQNAQMSQEDNHLSTNTVSQDNREROHNDNR-SLGHPEPLSNRPOGNSRQ 61

Db 24 ESPPRSCQEGRGQDEDENTAQMRSQNEDEEDPRRYVCSGP-----GRPG---- 74

QY 62 VVEODEEDELTKYGAKHVIMLFVPTLCMNVVATIKSVFTRKDGQILYPTPED 121

Db 75 -----LEBELTKYGAKHVIMLFVPTLCMIVVATIKSVFTRKNGQILYPTPED 127

QY 122 TETVGORALHSLNAAIMISIVVMTLLVLYKYRCYKVIHAWLIISLILFFESFTY 181

Db 128 TPVSGORLLNSVLTLMISIVVMTIFLVLYKYRCYKFIHGMILMSLMLFFTYIY 187

QY 182 LGEVKTYNVADVITVALLIMNLGVGMISIHMKGPLRLQOAYLIMISALMALVFIKYL 241

Db 188 LGEVKTYNVADVITVALLIMNLGVGMISIHMKGPLRLQOAYLIMISALMALVFIKYL 247

QY 242 PWTAMLLAVISYVDLAVLCPRKPLMLVETAOERNETLFPALITYSTWVLVMAEG 301

Db 248 PEMSAMVILGALSVDLAVLCPRKPLMLVETAOERNETLFPALITYSSAMVWVGMAKL 307

QY 302 DPEAQRVSKNSKYAESTERESQDTVAENDDGFSEEMEAQRDHLGPHRSTPESRAV 361

Db 308 DPSSGAL--QLPYDPE--MEEDSYDSFGE---PSYFEVEEPPLTGPG----- 349

QY 362 QELSSSILAGEPDEERGKVLGIDFIIFYSVLGGKASATASGDMNTTICFVALILGLCT 421

Db 360 EEL-----EEBERGKVLGIDFIIFYSVLGGKAAATGSGDMNTTICFVALILGLCT 402

QY 422 LLLAIFKKALPALPISITFGILVFYFADYLVOPMDOLAFHOFYI 467

Db 403 LLLAVFKKALPALPISITFGILIFYSTDNLVPRPMDTLASHOLYI 448

RESULT 13

US-09-754-949-6

Sequence 6, Application US/09754949

Patent No. US20020015939A1

GENERAL INFORMATION:

APPLICANT: MCCARTHY, JUSTIN

APPLICANT: CORDELL, BARBARA

TITLE OF INVENTION: METHODS FOR IDENTIFYING INHIBITORS OF

TITLE OF INVENTION: NEURONAL DEGENERATION

FILE REFERENCE: SCIOS.012A

QY 3 ELPAALSYFQNAQMSQEDNHLSTNTVSQDNREROHNDNR-SLGHPEPLSNRPOGNSRQ 61

Db 24 ESPPRSCQEGRGQDEDENTAQMRSQNEDEEDPRRYVCSGP-----GRPG---- 74

QY 62 VVEODEEDELTKYGAKHVIMLFVPTLCMNVVATIKSVFTRKDGQILYPTPED 121

Db 75 -----LEBELTKYGAKHVIMLFVPTLCMIVVATIKSVFTRKNGQILYPTPED 127

QY 122 TETVGORALHSLNAAIMISIVVMTLLVLYKYRCYKVIHAWLIISLILFFESFTY 181

Db 128 TPVSGORLLNSVLTLMISIVVMTIFLVLYKYRCYKFIHGMILMSLMLFFTYIY 187

QY 182 LGEVKTYNVADVITVALLIMNLGVGMISIHMKGPLRLQOAYLIMISALMALVFIKYL 241

Db 188 LGEVKTYNVADVITVALLIMNLGVGMISIHMKGPLRLQOAYLIMISALMALVFIKYL 247

QY 242 PWTAMLLAVISYVDLAVLCPRKPLMLVETAOERNETLFPALITYSTWVLVMAEG 301

Db 248 PEMSAMVILGALSVDLAVLCPRKPLMLVETAOERNETLFPALITYSSAMVWVGMAKL 307

QY 302 DPEAQRVSKNSKYAESTERESQDTVAENDDGFSEEMEAQRDHLGPHRSTPESRAV 361

Db 308 DPSSGAL--QLPYDPE--MEEDSYDSFGE---PSYFEVEEPPLTGPG----- 349

QY 362 QELSSSILAGEPDEERGKVLGIDFIIFYSVLGGKASATASGDMNTTICFVALILGLCT 421

Db 360 EEL-----EEBERGKVLGIDFIIFYSVLGGKAAATGSGDMNTTICFVALILGLCT 402

QY 422 LLLAIFKKALPALPISITFGILVFYFADYLVOPMDOLAFHOFYI 467

Db 403 LLLAVFKKALPALPISITFGILIFYSTDNLVPRPMDTLASHOLYI 448

RESULT 14

US-09-895-035-1

Sequence 1, Application US/09895035

Patent No. US2002008221A1

GENERAL INFORMATION:

APPLICANT: Patterson, Chandra

APPLICANT: Murry, Lynn E.

APPLICANT: Kaser, Matthew R.

TITLE OF INVENTION: HUMAN PRESENTIN VARIANT

FILE REFERENCE: PC-0047 CIP

CURRENT APPLICATION NUMBER: US/09/895,035

PRIOR FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: 09/116,640

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PERL Program

SEQ ID NO 1

LENGTH: 180

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc.feature

OTHER INFORMATION: Incyte ID No. US2002008221A1 1353337CDI

US-09-895-035-1

Query Match 33.4%; Score 798.5; DB 10; Length 180;

Best Local Similarity - 89.6%; Pred. NO. 1.4e-64;
Matches 164; Conservative 3; Mismatches 7; Indels 9; Gaps 3;

QY 1 MTELPAPLSTFQNAMQSEDNHLSNTVRSQNDNREREHDNRKSLGHPELSNGRQGNSR 60
Db 1 MTELPAPLSTFQNAMQSEDNHLSNT ---NDNREREHDNRKSLGHPELSNGRQGNSR 56			

DQ
61 QVEEQDEEEBELTKYGAHIMLFVPTLCMVVAATIKSVSFTRKDGOLITPTE 120

Db
57 QVEEQDEEBELTKYGAKHYMLFVPNTCMVVAVATIKSVSFTRKDGLITPPTE 116

```
OY      121 DTEVGQRALHSILNNAIMISIVVMTLLLVLYKRCVKVIHAMLISSLLLLFFSF I 180C
        ||||| |
DB       117 DTEVGQRALHSILNNAIMISIVVMTLLLVLYKRCVKVS--MRHRSLSLTF--FL 171I
        ||||| : ||| :
```

QY	181	YLG	183
Db	172	WLG	174

RESULT 15

US-09-823-153-8
Sequence 8, Application US/09823153

; GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb company

APPLICANT: Pak, Roger

APPLICANT: Lewis, Marc

APPLICANT: Smith, David

APPLICANT: Hendrick, Joseph
APPLICANT: Vintsky, Alexander

APPLICANT: Vinnitsky, Alexander

TITLE OF INVENTION: METHODS FOR

; FILE REFERENCE: D0004

CURRENT APPLICATION NUMBER
CURRENT FILING DATE

CURRENT FILING DATE: 2001-07-02
NUMBER OF SEQ ID NOS: 11

```

; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0

```

SEQ ID NO 8

LENGTH: 354

TYPE: PRT
ORGANISM: A

ORGANISM: *Aspergillus*
FEATURE:

NAME/KEY: misc_feature

[illegible]

US-09-823-153-8

Query Match	27.68:	Score 659.5:	DB 10:	Length 354:
-------------	--------	--------------	--------	-------------

Best Local Site

Matches	138;	Conservative	7;	Mismatches	8;	Indels	29;	Gaps	4;
---------	------	--------------	----	------------	----	--------	-----	------	----

Qy 239 KYL-PEPTAMLLILAVISY-----DLVAVLCPKPKPLRLMLVETAQENNETLFPALI 287
 ||| :: || : : ||| | : |||||
 Db 191 KYLKSSKYLAMPLOGMQATFCGGDHPKSDLV---PRG-----SLFPALI 232

[illegible]

Qy	348 LGHRSTPSRAAVQLSSSLIAGEDDEERGVKLGIDFIYSVLVGKASATASGDMNTT 4077
Db	293 LGHIRSTPSRAAVQLSSSLIAGEDDEERGVKLGIDFIYSVLVGKASATASGDMNTT 3522

QY	408	IA	409
Db	353	IA	354

Search completed: March 14, 2003, 20:13:57
Job time : 20 secs

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 19:20:34 ; Search time 27 Seconds
(Without alignments)
1662.769 Million cell updates/sec

Title: US-09-689-159A-2
Perfect score: 2391
Sequence: 1 MTELPAPLSTYFQNAQMSQEDN.....ATDYLVQPFMDQLAFHQFYI 467

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: / 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2387	98.6	467	2	SS8396
2	2357	98.6	463	2	presentin 1, sp1i
3	2275	95.1	467	2	presentin 1-463 -
4	2245	93.9	463	2	JC5080
5	2237	93.6	467	2	JC5081
6	1804	75.4	433	2	178388
7	1593	66.6	374	2	JC5390
8	1460.5	61.1	449	2	S63684
9	1453	60.8	448	2	JC5381
10	1391.5	57.8	442	2	AS6993
11	1059.5	44.3	836	2	139174
12	968.5	40.5	461	2	ES8453
13	546.5	22.9	453	2	S60253
14	539	22.5	397	2	T00724
15	511	21.4	358	2	A84702
16	312.5	13.1	465	2	T15184
17	125.5	5.2	2386	2	T27885
18	123.5	5.2	455	2	T39911
19	120.5	5.0	309	2	H9237
20	118.5	5.0	323	2	H90548
21	115.5	4.8	339	2	A48997
22	114	4.7	601	2	C71132
23	112	4.7	601	2	B84291
24	110.5	4.6	598	2	T52004
25	110	4.6	601	2	T05130
26	109	4.6	389	2	JH0170
27	108.5	4.5	389	2	AE1747
28	108	4.5	364	2	S46118
29	107.5	4.5	887	2	D95959
					MS277 homolog fil

30	104	4.3	599	2	T24333	hypothetical prote
31	103.5	4.3	470	2	T49272	hypothetical prote
32	103.5	4.3	477	2	D84306	sodium- and chlori
33	103	4.3	578	2	D87374	Rasa secretion sys
34	102.5	4.3	682	2	T43282	G protein-linked a
35	102	4.3	398	2	B82894	conserved hypotet
36	102	4.3	547	2	T33437	hypothetical prote
37	102	4.3	707	2	T09340	hypothetical prote
38	101.5	4.2	721	2	AH3417	lpsa protein limpo
39	101.5	4.2	1492	2	A39322	cystic fibrosis tr
40	101	4.2	389	2	AD1378	cell division prot
41	101	4.2	500	2	S12899	nicotinic acetylch
42	101	4.2	651	2	T46050	hypothetical prote
43	100.5	4.2	873	2	C90594	protein-export mem
44	100.5	4.2	1148	2	H90175	NMDH dehydrogenase
45	100	4.2	451	2	A96920	probable ABC trans

ALIGNMENTS

RESULT 1
S58396
presentin 1, splice form 467 - human
N:Alternate names: Alzheimer's disease protein 3; protein S182
C:Species: Homo sapiens (man)
C>Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 29-Sep-1999
C:Accession: S58396; S71401; S71402
R:Sherrington, R.; Rogaev, E.I.; Liang, Y.; Rogaeva, E.A.; Levesque, G.; Ikeda, M.; C
ero, I.; Pinessi, L.; Nee, L.; Chinakov, I.; Pollen, D.; Brookes, A.; Sanseau, P.; Po
E.; Romen, J.M.; St George-Hyslop, P.H.
Nature 375, 754-760, 1995
A:Title: Cloning of a gene bearing missense mutations in early-onset familial Alzheim
A:Reference number: 158025; MIM:95319502; PMID:7596406
A:Accession: S58396
A:Molecule type: mRNA
A:Residues: 1-467 <SHR>
A:Cross-references: EMBL:LA2110; NID:9904118; PIDN:ABA6416.1; PID:9904119
R:Vidal, R.; Ghiso, J.; Wisniewski, T.; Frangione, B.
FEBS Lett. 393, 19-23, 1996
A:Title: Alzheimer's presentin 1 gene expression in platelets and megakaryocytes. Id
A:Reference number: S71401; MIM:96397521; PMID:8804415
A:Accession: S71401
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 24-32;254-256,290-292;316-317,376-379.<VIN>
A:Cross-references: GDB:135682; OMIM:104311
A:Experimental source: Dami megakaryotic cell line (ATCC CRL-9792) and platelets
C:Genetics:
A:Gene: GDB:PSEN1; AD3; FAD; S182; PS1
A:Cross-references: GDB:135682; OMIM:104311
A:Map position: 14q24.3-14q24.3
C:Superfamily: presentin
C:Keywords: alternative splicing; Alzheimer's disease; glycoprotein; transmembrane pr
F:82-100/Domain: transmembrane #status predicted <TM1>
F:133-134/Domain: transmembrane #status predicted <TM2>
F:164-185/Domain: transmembrane #status predicted <TM3>
F:195-213/Domain: transmembrane #status predicted <TM4>
F:221-238/Domain: transmembrane #status predicted <TM5>
F:244-264/Domain: transmembrane #status predicted <TM6>
F:281-301/Domain: transmembrane #status predicted <TM7>
F:408-428/Domain: transmembrane #status predicted <TM8>
F:433-453/Domain: transmembrane #status predicted <TM9>
F:279,405/Binding site: carboxylate (Asn) (covalent) #status predicted
Query Match 99.8%; Score 2387; DB 2; Length 467;
Best Local Similarity 99.8%; Pred. No. 1.5e-178;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Db 61 QVVEDEDEDELTLYGAKHVMLEFVPTLCVVVAVATIKSVFTRDGOGLITPFE 120
QY 121 DFEVGOARLHSLNAIMISIVVMTLLVLYKRCYKVIHAWLIISLLLEFFSFI 180
Db 121 DFEVGOARLHSLNAIMISIVVMTLLVLYKRCYKVIHAWLIISLLLEFFSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLIMNGVGMISIHMKGPLRLOQAVLIMISALMAVFIKY 240
Db 181 YLGEVFKTYNVAVDYITVALLIMNGVGMISIHMKGPLRLOQAVLIMISALMAVFIKY 240
QY 241 LPEWTAMLILAVISYVDLVAVLCPRKPLRMVETAOERNETLFPALITYSTWMLVNNAE 300
Db 241 LPEWTAMLILAVISYVDLVAVLCPRKPLRMVETAOERNETLFPALITYSTWMLVNNAE 300
QY 301 GDEPAORRYSKSKNAESTERESODTVAENDDGFSEMEAROSHLGPHRSTPESRAA 360
Db 301 GDEPAORRYSKSKNAESTERESODTVAENDDGFSEMEAROSHLGPHRSTPESRAA 360
QY 361 VOELSSSIAGDEPBERGVKLGIDFIFYSVLVGKASATASGDMWTTTACFAVAILIGLCL 420
Db 361 VOELSSSIAGDEPBERGVKLGIDFIFYSVLVGKASATASGDMWTTTACFAVAILIGLCL 420
QY 421 TLLLAIFKKALPALPISTFGVLFYFATDYLVOPMDQLAFHOEYI 467
Db 421 TLLLAIFKKALPALPISTFGVLFYFATDYLVOPMDQLAFHOEYI 467
```

RESULT 2

```
S63683
C:Species: Homo sapiens (man)
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999
C:Accession: S63683
R:Sahara, N.; Yahagi, Y.; Takagi, H.; Kondo, T.; Okochi, M.; Usami, M.; Shirasawa, T.; N
FEBS Lett. 381, 7-11, 1996
A:Title: Identification and characterization of presentin I-467, I-463 and I-374.
A:Reference number: S63683; MUID:96193901; PMID:8641442
A:Accession: S63683
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-463 <SAB>
A:Cross-references: EMBL:U40379; NID:g1244637; PIDD:AAB05894.1; PID:g1244638
C:Superfamily: presentin
```

```
Query Match 98.6%; Score 2357; DB 2; Length 463;
Best Local Similarity 98.9%; Pred. No. 3.2e-176;
Matches 462; Conservative 0; Mismatches 1; Indels 4; Gaps 1;
```

```
QY 1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDNREROENHNRSLGHPPELSNGRPOGNSR 60
Db 1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDNREROENHNRSLGHPPELSNGRPOGNSR 56
QY 61 QVVEDEDEDELTLYGAKHVMLEFVPTLCVVVAVATIKSVFTRDGOGLITPFE 120
Db 61 QVVEDEDEDELTLYGAKHVMLEFVPTLCVVVAVATIKSVFTRDGOGLITPFE 116
QY 121 DFEVGOARLHSLNAIMISIVVMTLLVLYKRCYKVIHAWLIISLLLEFFSFI 180
Db 121 DFEVGOARLHSLNAIMISIVVMTLLVLYKRCYKVIHAWLIISLLLEFFSFI 176
QY 181 YLGEVFKTYNVAVDYITVALLIMNGVGMISIHMKGPLRLOQAVLIMISALMAVFIKY 240
Db 181 YLGEVFKTYNVAVDYITVALLIMNGVGMISIHMKGPLRLOQAVLIMISALMAVFIKY 236
QY 241 LPEWTAMLILAVISYVDLVAVLCPRKPLRMVETAOERNETLFPALITYSTWMLVNNAE 300
Db 241 LPEWTAMLILAVISYVDLVAVLCPRKPLRMVETAOERNETLFPALITYSTWMLVNNAE 296
QY 301 GDEPAORRYSKSKNAESTERESODTVAENDDGFSEMEAROSHLGPHRSTPESRAA 360
Db 301 GDEPAORRYSKSKNAESTERESODTVAENDDGFSEMEAROSHLGPHRSTPESRAA 356
```

```
QY 361 VOELSSSIAGDEPBERGVKLGIDFIFYSVLVGKASATASGDMWTTTACFAVAILIGLCL 420
Db 357 VOELSSSIAGDEPBERGVKLGIDFIFYSVLVGKASATASGDMWTTTACFAVAILIGLCL 416
QY 421 TLLLAIFKKALPALPISTFGVLFYFATDYLVOPMDQLAFHOEYI 467
Db 417 TLLLAIFKKALPALPISTFGVLFYFATDYLVOPMDQLAFHOEYI 463
```

RESULT 3

J05080

```
presentin 1 protein isoform 467 - lesser mouse lemur
C:Species: Microcebus murinus (lesser mouse lemur)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 20-Jun-2000
C:Accession: J05080
R:Calenda, A.; Mestre-Frances, N.; Czech, C.; Pradier, L.; Pelter, A.; Bons, N.; Bell
Biochem. Biophys. Res. Commun. 228, 430-439, 1996
A:Title: Molecular cloning, sequencing, and brain expression of the presentin 1 gene
A:Reference number: J05080; MUID:97079199; PMID:8920931
A:Accession: J05080
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
```

A:Residues: 1-467 <CAL>

```
A:Cross-references: EMBL:271333; NID:g1707591; PIDD:CA95930.1; PID:g1707592
A:Experimental source: brain
C:Comment: This protein is an integral membrane protein with seven transmembrane dom
C:Genetics:
A:Gene: ps1
A:Map position: 14
```

C:Superfamily: presentin

```
C:Keywords: transmembrane protein
F:82-100/Domain: transmembrane #status predicted <TM1>
F:133-154/Domain: transmembrane #status predicted <TM2>
F:164-185/Domain: transmembrane #status predicted <TM3>
F:195-213/Domain: transmembrane #status predicted <TM4>
F:221-238/Domain: transmembrane #status predicted <TM5>
F:244-261/Domain: transmembrane #status predicted <TM6>
F:408-428/Domain: transmembrane #status predicted <TM7>
```

```
Query Match 95.1%; Score 2275; DB 2; Length 467;
Best Local Similarity 94.9%; Pred. No. 8e-170;
Matches 443; Conservative 11; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDNREROENHNRSLGHPPELSNGRPOGNSR 60
Db 1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDNREROENHNRSLGHPPELSNGRPOGNSR 60
QY 61 QVVEDEDEDELTLYGAKHVMLEFVPTLCVVVAVATIKSVFTRDGOGLITPFE 120
Db 61 QVVEDEDEDELTLYGAKHVMLEFVPTLCVVVAVATIKSVFTRDGOGLITPFE 120
QY 121 DFEVGOARLHSLNAIMISIVVMTLLVLYKRCYKVIHAWLIISLLLEFFSFI 180
Db 121 DFEVGOARLHSLNAIMISIVVMTLLVLYKRCYKVIHAWLIISLLLEFFSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLIMNGVGMISIHMKGPLRLOQAVLIMISALMAVFIKY 240
Db 181 YLGEVFKTYNVAVDYITVALLIMNGVGMISIHMKGPLRLOQAVLIMISALMAVFIKY 240
QY 241 LPEWTAMLILAVISYVDLVAVLCPRKPLRMVETAOERNETLFPALITYSTWMLVNNAE 300
Db 241 LPEWTAMLILAVISYVDLVAVLCPRKPLRMVETAOERNETLFPALITYSTWMLVNNAE 300
QY 301 GDEPAORRYSKSKNAESTERESODTVAENDDGFSEMEAROSHLGPHRSTPESRAA 360
Db 301 GDEPAORRYSKSKNAESTERESODTVAENDDGFSEMEAROSHLGPHRSTPESRAA 360
QY 361 VOELSSSIAGDEPBERGVKLGIDFIFYSVLVGKASATASGDMWTTTACFAVAILIGLCL 420
Db 361 VOELSSSIAGDEPBERGVKLGIDFIFYSVLVGKASATASGDMWTTTACFAVAILIGLCL 420
QY 421 TLLLAIFKKALPALPISTFGVLFYFATDYLVOPMDQLAFHOEYI 467
Db 421 TLLLAIFKKALPALPISTFGVLFYFATDYLVOPMDQLAFHOEYI 467
```

Db 421 TLLLAIFKKALPALPISITFGLVFEFATDYLVOPFMDQLAFHQFYI 467

RESULT 4

presentin1n 1 protein isoform 463 - lesser mouse lemur
C:Species: Microcebus murinus (lesser mouse lemur)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 13-Sep-1998
C:Accession: J05081
R:Calenda, A.; Mestre-Frances, N.; Czech, C.; Pradler, L.; Petter, A.; Bons, N.; Bellis, Biochem. Biophys. Res. Commun. 228, 430-439, 1996
A:Title: Molecular cloning, sequencing, and brain expression of the presentin1 gene in A:Reference number: J05080; MUID:97079199; PMID:8920931
A:Contents: brain
A:Accession: J05081
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-463 <CAL>
A:Cross-references: EMBL:271333
C:Comment: This protein is an intermembrane protein with seven transmembrane domains. It C:Genetics:
A:Gene: psi1
A:Map position: 14
C:Superfamily: presentin1n
C:Keywords: transmembrane protein
F:78-96/Domain: transmembrane #status predicted <TM1>
F:129-150/Domain: transmembrane #status predicted <TM2>
F:160-181/Domain: transmembrane #status predicted <TM3>
F:191-209/Domain: transmembrane #status predicted <TM4>
F:217-234/Domain: transmembrane #status predicted <TM5>
F:240-257/Domain: transmembrane #status predicted <TM6>
F:404-424/Domain: transmembrane #status predicted <TM7>

Query Match 93.9%; Score 2245; DB 2; Length 463;
Best Local Similarity 94.0%; Pred. No. 1.7e-167;
Matches 439; Conservative 11; Mismatches 13; Indels 4; Gaps 1;

QY 1 MTELPAPLSTYFQNAQMSQDNHLSNTVRSQNDKREQENHNDRLSLGHPPLSLNGRQNSR 60
Db 1 MTELPAPLSTYFQNAQMSQDNHLSNT-----NDNREGQDHDRRLGNPEPLSLNGRQNSG 56
QY 61 QVEODEDEDEBELTKYGAKHVIMLFVPTLCMVVAVATIKSVSYTRKQGLITPTPE 120
Db 57 PVEDEDEDEBELTKYGAKHVIMLFVPTLCMVVAVATIKSVSYTRKQGLITPTPE 116
QY 121 DTEYGOALHSILNAAMISIVVMTLLVLYKRCYKVIHAWLISSLLLEFFSPT 180
Db 117 DTEYGOALHSILNAAMISIVVMTLLVLYKRCYKVIHAWLISSLLLEFFSPT 176
QY 181 YLGEVFKTYNAVDYITVALLTNLGVVGMISIHKGPLRLOQAVLIMSALMAVFTKY 240
Db 177 YLGEVFKTYNAVDYITVALLTNLGVVGMISIHKGPLRLOQAVLIMSALMAVFTKY 236
QY 241 LPEWTAMLILAVISYDVAVLCPRGPLMLVETAOERETLFPALITYSTWMLVNNAE 300
Db 237 LPEWTAMLILAVISYDVAVLCPRGPLMLVETAOERETLFPALITYSTWMLVNNAE 296
QY 301 GDPKQRRVSKNSKNAESTERESQDYVAENDGCFSEEMKQORSHLCPHRSTPESRAA 360
Db 297 GDPKQRRVSKNSKNAESTERESQDYVAENDGCFSEEMKQORSHLCPHRSTPESRAA 356
QY 361 VOELSSSILAGDPERGVKTLGDFIFYSVLVGKASATASGDMWTTTACFAAILIGLCL 420
Db 357 VOELSSSILAGDPERGVKTLGDFIFYSVLVGKASATASGDMWTTTACFAAILIGLCL 416
QY 421 TLLLAIFKKALPALPISITFGLVFEFATDYLVOPFMDQLAFHQFYI 467
Db 417 TLLLAIFKKALPALPISITFGLVFEFATDYLVOPFMDQLAFHQFYI 463

RESULT 5
178388
5182 protein - mouse

C:Species: Mus musculus (house mouse)
C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 29-Sep-1999
C:Accession: I78388

R:Sherrington, R.; Rogaev, E.I.; Liang, Y.; Rogaeva, E.A.; Levesque, G.; Ireda, M.; C E.O.; I.; Pliness, L.; Nee, L.; Chumakov, I.; Pollen, D.; Brookes, A.; Sansau, P.; Po E.; Romenens, J.M.; St George-Hyslop, P.H.
Nature 375, 754-760, 1995
A:Title: Cloning of a gene bearing missense mutations in early-onset familial Alzheimer A:Reference number: I58095; MUID:95319502; PMID:7596406

A:Accession: I78388
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-467 <RES>
A:Cross-references: GB:I42177; NID:g904129; PIDN:AA02094.1; PID:g904130

C:Superfamily: presentin1n
Query Match 93.6%; Score 2237; DB 2; Length 467;
Best Local Similarity 92.5%; Pred. No. 7.4e-167;
Matches 432; Conservative 18; Mismatches 17; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFQNAQMSQDNHLSNTVRSQNDKREQENHNDRLSLGHPPLSLNGRQNSR 60
Db 1 MTELPAPLSTYFQNAQMSQDNHLSNTVRSQNDKREQENHNDRLSLGHPPLSLNGRQNSR 60
QY 61 QVEODEDEDEBELTKYGAKHVIMLFVPTLCMVVAVATIKSVSYTRKQGLITPTPE 120
Db 61 QVEODEDEDEBELTKYGAKHVIMLFVPTLCMVVAVATIKSVSYTRKQGLITPTPE 120
QY 121 DTEYGOALHSILNAAMISIVVMTLLVLYKRCYKVIHAWLISSLLLEFFSPT 180
Db 121 DTEYGOALHSILNAAMISIVVMTLLVLYKRCYKVIHAWLISSLLLEFFSPT 180
QY 181 YLGEVFKTYNAVDYITVALLTNLGVVGMISIHKGPLRLOQAVLIMSALMAVFTKY 240
Db 181 YLGEVFKTYNAVDYITVALLTNLGVVGMISIHKGPLRLOQAVLIMSALMAVFTKY 240
QY 241 LPEWTAMLILAVISYDVAVLCPRGPLMLVETAOERETLFPALITYSTWMLVNNAE 300
Db 241 LPEWTAMLILAVISYDVAVLCPRGPLMLVETAOERETLFPALITYSTWMLVNNAE 300
QY 301 GDPKQRRVSKNSKNAESTERESQDYVAENDGCFSEEMKQORSHLCPHRSTPESRAA 360
Db 301 GDPKQRRVSKNSKNAESTERESQDYVAENDGCFSEEMKQORSHLCPHRSTPESRAA 360
QY 361 VOELSSSILAGDPERGVKTLGDFIFYSVLVGKASATASGDMWTTTACFAAILIGLCL 420
Db 361 VOELSSSILAGDPERGVKTLGDFIFYSVLVGKASATASGDMWTTTACFAAILIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGLVFEFATDYLVOPFMDQLAFHQFYI 467
Db 421 TLLLAIFKKALPALPISITFGLVFEFATDYLVOPFMDQLAFHQFYI 467

RESULT 6
J05390
presentin1n-alpha - African clawed frog

C:Species: Xenopus laevis (African clawed frog)
C:Date: 04-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000
C:Accession: J05390
R:Tsujimura, A.; Yasojima, K.; Hashimoto-Gotoh, T.
Biochem. Biophys. Res. Commun. 231, 392-396, 1997

A:Title: Cloning of Xenopus presentin1n-alpha and -beta cDNAs and their differential e A:Reference number: J05390; MUID:97223465; PMID:9070286
A:Accession: J05390
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-433 <TSU>
A:Cross-references: DBJ:D84427; NID:G1944353; PIDN:BAA19570.1; PID:G1944354

C:Superfamily: presentin1n
C:Comment: This protein plays a role in negative regulation of apoptotic cascades dur F:99-119/Domain: transmembrane #status predicted <TM2>

Db	247	IKYLPWSAMVILGAISVYDLAVLCBKPRLVETAQERNEPIFALITYSSAMMTVG	306
QY	298	MAEGDPEAQRVSKSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPES	357

Db 307 MAD-SATADGEMNOVOYHIDNTEPGANSTV-----ED 338
QY 358 RAAVOELSSSLAGEDP-EERGVKLGDFIFYSVLVGKASATASGDMNTTACFAVAILIGLCT 416
Db 339 AAEFRIGQISMLSEDDPEERGVKLGDFIFYSVLVGKAAATASGDMNTTACFAVAILI 398
QY 417 GLCLTLLLAIFKALPALPISITFGIYFVATDYLVOPEMDQAHOFYI 467
Db 399 GLCLTLLLAIFKALPALPISITFGIYFVATDYLVOPEMDQAHOFYI 449

RESULT 9

presentin 2 - human
N:Alternate names: Alzheimer's disease protein 4
C:Species: Homo sapiens (man)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 17-Nov-2000
C:Accession: A56993; 158098
R:Levy-Lahad, E.; Masco, W.; Poorkaj, P.; Romano, D.M.; Oshima, J.; Pettingell, W.H.; Yu
Science 269, 973-977, 1995
A:Title: Candidate gene for the chromosome 1 familial Alzheimer's disease locus.
A:Reference number: A56993; MUID:95365816; PMID:7638622
A:Accession: A56993
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-448 <RES>
A:Cross-references: GB:L43964; NID:9951202; PIDN:AAB59557.1; PID:9951203
R:Rogaev, E.I.; Shadmehr, R.; Rogaeva, E.A.; Levesque, G.; Ikeda, M.; Liang, Y.; Chit,
Cohen, B.; Lannfelt, L.; Frieser, P.E.; Kommens, J.M.; St George-Hyslop, P.H.
Nature 376, 775-778, 1995
A:Title: Familial Alzheimer's disease in kindreds with missense mutations in a gene on C
A:Reference number: 158098; MUID:95379971; PMID:7651536
A:Accession: 158098
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-122; P, 124-448 <RE2>
A:Cross-references: GB:L44577; NID:9950347; PIDN:AAC42012.1; PID:9950348
C:Genetics:
A:Gene: GDB:PSEN2; AD4; STM2; PS2; E5-1
A:Cross-references: GDB:633044; OMIM:600759
A:Map position: 1q31-1q42
C:Superfamily: presentin 2

Query Match 50.8%; Score 1453; DB 2; Length 448;
Best Local Similarity 65.2%; Pred. No. 1,1e-105;
Matches 304; Conservative 89; Mismatches 81; Indels 42; Gaps 8;

QY 3 ELPAFLSYFQNAQSEDMHLSNTVRSQDNREQEHNDNR-SLGHPEPLSNGRPGNSRQ 61
Db 24 ESPPRSCQEGRGPEDEENTAMRQSENEDEDEDPDYVCSGVP-----GRPG----- 74
QY 62 VVEDDEDEDELTKYGAHVMFVPTLCMVVVVATIKSVFTRKDGOLITPTPTED 121
Db 75 -----LEELTLTKYGAHVMFVPTLCMVVVVATIKSVFTRKDGOLITPTPTED 127
QY 122 TETVGORALHSILNAAMISIVVMTILVLYKRCYKRVHAWLISSLLLEFFSFYI 181
Db 128 TPTVGQRILNSVMTLIMISIVVMTIFLVLYKRCYKRVHAWLISSLLLEFFSFYI 187
QY 182 LGEVFKTYNVAVDYITVALLIMNLGVGMISIHMKGPLRLDOAVYIMISALMALVFIY 241
Db 188 LGEVFKTYNVAVDYITVALLIMNLGVGMISIHMKGPLRLDOAVYIMISALMALVFIY 247
QY 242 PEMTAMILAVISYVDIAVLCPRGLMLVETAOERNEETFPALITVSTWVLMVMAEG 301
Db 248 PEMTAMILAVISYVDIAVLCPRGLMLVETAOERNEETFPALITVSTWVLMVMAEG 307
QY 302 DPEAQRYSKSKYNAESTERESODTVAENDDGFSEEMEARSDSHLGRHSTPESRAV 361
Db 308 DPEAQRYSKSKYNAESTERESODTVAENDDGFSEEMEARSDSHLGRHSTPESRAV 349
QY 362 QELSSSILAGEDPEERGVKLGDFIFYSVLVGKASATASGDMNTTACFAVAILIGLCT 421
Db 362 QELSSSILAGEDPEERGVKLGDFIFYSVLVGKASATASGDMNTTACFAVAILIGLCT 421

Db 350 EEL-----DEERGVKLGDFIFYSVLVGKAAATASGDMNTTACFAVAILIGLCT 402
QY 422 LLLAIFKALPALPISITFGIYFVATDYLVOPEMDQAHOFYI 467
Db 403 LLLAIFKALPALPISITFGIYFVATDYLVOPEMDQAHOFYI 448

RESULT 10

seven trans-membrane domain protein AD3LP/AD5 - human
C:Species: Homo sapiens (man)
C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 29-Sep-1999
C:Accession: I39174
R:Li, J.; Ma, J.; Potter, H.
Proc. Natl. Acad. Sci. U.S.A. 92, 12180-12184, 1995
A:Title: Identification and expression analysis of a potential familial Alzheimer's d
A:Reference number: I39174; MUID:96109229; PMID:8618867
A:Accession: I39174
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-442 <RES>
A:Cross-references: EMBL:U34349; NID:91079575; PIDN:AAC50290.1; PID:91079576
C:Superfamily: presentin 2

Query Match 57.8%; Score 1381.5; DB 2; Length 442;
Best Local Similarity 64.4%; Pred. No. 4e-100;
Matches 289; Conservative 39; Mismatches 80; Indels 41; Gaps 8;

QY 3 ELPAFLSYFQNAQSEDMHLSNTVRSQDNREQEHNDNR-SLGHPEPLSNGRPGNSRQ 61
Db 24 ESPPRSCQEGRGPEDEENTAMRQSENEDEDEDPDYVCSGVP-----GRPG----- 74
QY 62 VVEDDEDEDELTKYGAHVMFVPTLCMVVVVATIKSVFTRKDGOLITPTPTED 121
Db 75 -----LEELTLTKYGAHVMFVPTLCMVVVVATIKSVFTRKDGOLITPTPTED 127
QY 122 TETVGORALHSILNAAMISIVVMTILVLYKRCYKRVHAWLISSLLLEFFSFYI 181
Db 128 TPTVGQRILNSVMTLIMISIVVMTIFLVLYKRCYKRVHAWLISSLLLEFFSFYI 187
QY 182 LGEVFKTYNVAVDYITVALLIMNLGVGMISIHMKGPLRLDOAVYIMISALMALVFIY 241
Db 188 LGEVFKTYNVAVDYITVALLIMNLGVGMISIHMKGPLRLDOAVYIMISALMALVFIY 247
QY 242 PEMTAMILAVISYVDIAVLCPRGLMLVETAOERNEETFPALITVSTWVLMVMAEG 301
Db 248 PEMTAMILAVISYVDIAVLCPRGLMLVETAOERNEETFPALITVSTWVLMVMAEG 307
QY 302 DPEAQRYSKSKYNAESTERESODTVAENDDGFSEEMEARSDSHLGRHSTPESRAV 361
Db 308 DPEAQRYSKSKYNAESTERESODTVAENDDGFSEEMEARSDSHLGRHSTPESRAV 348
QY 362 QELSSSILAGEDPEERGVKLGDFIFYSVLVGKASATASGDMNTTACFAVAILIGLCT 421
Db 362 QELSSSILAGEDPEERGVKLGDFIFYSVLVGKASATASGDMNTTACFAVAILIGLCT 403
QY 422 LLLAIFKALPALPISITFGIYFVATDYLVOPEMDQAHOFYI 467
Db 404 LLLAIFKALPALPISITFGIYFVATDYLVOPEMDQAHOFYI 448

RESULT 11

protein F35H12.3 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
C:Accession: E89453
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A:Reference number: A75000; MUID:99065613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;

Db 309 PSASEHSTSVGT - RGNMEDRESVNDENMSPLVELMGMDNREARGLEESDNNVDISNKG 367
Oy 379 VKLIGDGFIEFYSVLVGRASATASGDMNTTACFAVAILGICLTLLLAIFKALPALPLS 438
Db 368 IKLIGADGTFISVLVGR---AMVDLMTVYACTYLAISGLCTLLSYNRALPALPLS 424
Oy 439 ITFGLVFFAYADYLVQPFM 457
Db 425 IMLGVFFELTRLMEPFV 443

RESULT 14
A84702
probable presentin [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: A84702
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-397 <SNO>
A:Cross-references: GB:AE002093; NID:94567215; PIDN:AD23630.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g29900
A:Map position: 2
C:Superfamily: presentin

Query Match 22.5%; Score 539; DB 2; Length 397;
Best Local Similarity 33.8%; Pred. No. 1.9e-34;
Matches 144; Conservative 79; Mismatches 145; Indels 58; Gaps 15;

Oy 52 NGRPGNSRQVVEDEDEDELTLYKAKHYMLFVPTLCVVVVAT-----KS 102
Db 4 NGRP-----RSLIDSLGE-----LAIITPVSICFTYVLLVLCILNSPSSS 47
Oy 103 VSEYTRKDGOLLYPTE-DTEVGORALHSLNAIMISVIVMTLLVLYKRYCYK 161
Db 48 ASF-----SIATAYSSESDDSSMDKFGALLNSVFAATVATFVLVLYKCYK 102
Oy 162 IHAMLISSLLFFSTYIGEVFKTYNAVDTYVALLVNLGVGMISHW-KGPIR 220
Db 103 LKFYGFSAFTVLMGGEIIVLLIDRRFPIDSTITFLILFNFSVGVFAVMSKFSIL 162
Oy 221 LQOAVLIMISALMALVFICYLPENTAWLILAVISYDVLAVICPKGPLMLVETAOEBNE 280
Db 163 ITQGLVIGVLA-YFTTLPEMTWLVLAALYDIAAVLLPVGPLRLVEMAISDE 221
Oy 281 TLPFALIVSTWVWLVNNAEGDPEAORRV---SKNSKYNAESTE-RESQDTVAENDDGF 336
Db 222 DI-PALVYEARPV---IRNDSRSVQRVVRQRRSSQNNANNENVRVVSASEVEEHGS 276
Oy 337 SEEMFAQDSHUGPHRSTP---ESRAVOELSSIIAGDEPBERG-VKLGDFITYSVLV 393
Db 277 SERAEI-----SVPLIDRPEQAENSETFLEGIGLSSGAIKLGLGFITYSVLV 326
Oy 394 GKASATASGDMNTTACFAVAILGICLTLLLAIFKALPALPLSITFGVYFATDVLV 453
Db 327 GRA---AMVDLMTVYACTYLAISGLCTLLSYNRALPALPLS 424
Oy 454 QPFMDQ 459
Db 384 EVFVVQ 389

RESULT 15
T15184
presentin-beta homolog - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: T15184; T42237
R:Connell, M.; Magill, L.
Submitted to the EMBL Data Library, April 1997
A:Description: The sequence of C. elegans cosmid C18E3.
A:Reference number: Z18304
A:Accession: T15184
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-358 <CON>
A:Cross-references: EMBL:AF000265; NID:g1947147; PID:g1947155; PIDN:AA852948.1; GSPDB
A:Experimental source: strain Bristol N2; clone C18E3
R:Lin, X.; Greenwald, I.
Proc. Natl. Acad. Sci. U.S.A. 94, 12204-12209, 1997
A:Title: HOP-1, a Caenorhabditis elegans presentin, appears to be functionally redun
A:Reference number: Z22112; MUID:98004548; PMID:9342387
A:Accession: T42237
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-358 <LIX>
A:Cross-references: EMBL:AF021905; NID:g2618986; PIDN:AA84394.1; PID:g2618987
C:Genetics:
A:Gene: HOP-1; CESP:C18E3.8
A:Map position: 1
A:Introns: 44/2; 85/3; 215/1; 263/1; 291/3

Query Match 21.4%; Score 511; DB 2; Length 358;
Best Local Similarity 30.8%; Pred. No. 2.6e-32;
Matches 118; Conservative 78; Mismatches 145; Indels 42; Gaps 7;

Oy 77 YGAKHVMFVPTLCMVVVATIKSVSFYTRKDGOLLYTP-TEDTEVGORALHSLIN 135
Db 8 YSGKITGVLPVATCMFVALINVLQSPQDQSKVYIGLHSTDTADSGTITLY----- 63
Oy 136 AAIMISVIVMTLLVLYKRYCYKVIHAMISSLLLFPSFTYLGVEFKTYNAVADY 195
Db 64 ---LIGLILITSLGFCQMKFYKAIKVVYLANSIGILVYSVHFQRIAGQSIPIVSV 120
Oy 196 ITVALLVNLGVGMISHWKGPLRLOQAYLIMISALMALVFICYLPENTAWLILAVISV 255
Db 121 PTFEFLIQFGIGITCLHMKSHRRLHOFYLLMAGLTAIFLITLIPDWTVMALTAISF 180
Oy 256 YDLVAVLCPKGPLMLVETAOERNETLFPALIVSTWVWLVNNAEGDPEAORRVSKSY 315
Db 161 WDIYAVLTPCGPLKMLVETANRRGDKFPAILYNSS-----SYNDEV 222
Oy 316 NAESTERESODTVAENDDGFSEWEAQRDSHUGPHRSTPESRAAVOELSSIIAGDEPE 375
Db 223 DSPDTRNSRTPLTFFNNSSSRLLLES--DSLRLP-PVPIRRIREVREGTI----- 272
Oy 376 ERGVKLGDFIEFYSVLVGRASATASGDMNTTACFAVAILGICLTLLLAIFKALPAL 435
Db 273 ---RLGMDGEFFYSIMLGNVTQC--PLPVTVACFVSNLVGLTITLPIVLSQTLPAL 326
Oy 436 PISITFGVYFATDYLQPFMD 458
Db 327 PPLIAIAIFFFSHIATLPFD 349

Search completed: March 14, 2003, 20:09:41
Job time : 40 secs

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OM protein - protein search, using sw model

Run on: March 14, 2003, 19:19:10 ; Search time 16 Seconds
(without alignments)
1210.590 Million cell updates/sec

Title: US-09-689-159A-2

Perfect score: 2391
Sequence: 1 MTELPAPLSYFQNAQMSQEDN.....ATDYLVQPMQLAFHQFYI 467

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt.40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	2387	99.8	467 1 PSN1_HUMAN	P49768 homo sapien
2	2275	95.1	467 1 PSN1_MICMU	P79802 microcebus
3	2237	93.6	467 1 PSN1_MOUSE	P49769 mus musculu
4	2209.5	92.4	468 1 PSN1_RAT	P97887 rattus norv
5	2184.5	91.4	478 1 PSN1_BOVIN	O94197 bos taurus
6	1804	75.4	433 1 PSN1_XENLA	O12976 xenopus lae
7	1461	61.1	448 1 PSN2_HUMAN	P49810 homo sapien
8	1460.5	61.1	449 1 PSN2_XENLA	O12977 xenopus lae
9	1449	60.6	445 1 PSN2_MICMU	P79801 microcebus
10	1441.5	60.3	449 1 PSN2_BOVIN	O94196 bos taurus
11	1439	60.2	448 1 PSN2_MOUSE	O61144 mus musculu
12	1439	60.2	448 1 PSN2_RAT	O86777 rattus norv
13	1177.5	49.2	541 1 PSN_DROME	O02194 drosophila
14	1059.5	44.3	444 1 PSN_CAEEL	P52166 caenorhabdi
15	546.5	22.9	453 1 PSNH_ARATH	O64668 arabidopsis
16	511	21.4	358 1 HOP1_CAEEL	O02100 caenorhabdi
17	312.5	13.1	465 1 SPE4_CAEEL	O01608 caenorhabdi
18	125.5	5.2	2386 1 RAD3_SCHRO	O02099 schizosacch
19	118.5	5.0	323 1 CD47_HUMAN	O08722 homo sapien
20	112	4.7	601 1 OAR_DROME	P22270 drosophila
21	108.5	4.5	488 1 YB91_YEAST	P36142 saccharomyc
22	107.5	4.4	971 1 P277_MYCPN	P73387 mycoplasma
23	105.5	4.4	436 1 A2AR_CARAU	P13251 carassius a
24	103.5	4.3	2365 1 CCAH_MOUSE	O86427 mus musculu
25	101.5	4.2	1492 1 CTRF_SQUAC	P26362 squallus aca
26	101	4.2	519 1 ACB4_DROME	P23162 drosophila
27	101	4.2	1580 1 ACCH_HUMAN	O09428 homo sapien
28	100	4.2	441 1 DIHR_ACHDO	O16983 acheta dome
29	99.5	4.2	970 1 Y277_MYCGE	O49409 mycoplasma
30	99	4.1	1581 1 ACC8_RAT	O09429 rattus norv
31	98.5	4.1	298 1 FTGL_YEAST	P36224 saccharomyc
32	98.5	4.1	385 1 CYB_ACACA	O37378 acanthamoeb
33	97.5	4.1	354 1 C3X1_MOUSE	O920d9 mus musculu

34	97	4.1	764 1 TSHR_MOUSE	P47750 mus musculu
35	97	4.1	776 1 CME3_BACCU	P39695 bacillus su
36	96.5	4.0	226 1 N16M_DICTI	O37314 dictyostell
37	96.5	4.0	763 1 TSHR_BOVIN	O27987 bos taurus
38	96	4.0	458 1 N04M_PETNA	O35542 petromyzon
39	95	4.0	522 1 C822_SOYBN	O81972 glycine max
40	95	4.0	628 1 YEH5_YEAST	P39980 saccharomyc
41	95	4.0	672 1 HYFB_ECOLI	P23482 escherichia
42	95	4.0	871 1 Y47D_SCHRO	O09766 schizosacch
43	95	4.0	944 1 MM13_MYCPN	O53657 mycobacteri
44	95	4.0	1558 1 YK83_YEAST	P36028 saccharomyc
45	94	3.9	294 1 OPPC_LACLA	O07743 lactococcus

ALIGNMENTS

RESULT 1
ID PSN1_HUMAN STANDARD: PRT: 467 AA.
AC P49768: 014762: 015719: 015720:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Presentin 1 (PS-1) (S182 protein).
GN PSN1 OR PSN1 OR AD3 OR PSL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS AD (ISOFORMS I-467 AND I-463).
RC TISSUE-Brain.
RX MEDLINE=95319502; PubMed=7596406;
RA Sherrington R., Rogeev E.I., Liang Y., Rogeeva E.A., Levesque G.,
RA Ikeda M., Chi H., Lin C., Li G., Holman K., Tsuda T., Mar L.,
RA Foncin J.-F., Brunl A.C., Montesi M.P., Sorbi S., Ralnero I.,
RA Saneau P., Nee L., Chumakov I., Pollen D., Brookes A.,
RA Perleak-Vance M.A., Tanzi R.E., Roses A.D., Fraser P.E.,
RA Rommens J.M., St George-Hyslop P.H.;
RT "Cloning of a gene bearing missense mutations in early-onset familial
RT Alzheimer's disease.";
RL Nature 375:754-760(1995).
[2]
RN SEQUENCE FROM N.A. (ISOFORMS I-463 AND I-374).
RC TISSUE-Blood, and Brain.
RX MEDLINE=96193901; PubMed=8641442;
RA Sahara N., Yahagi Y.-I., Takagi H., Kondo T., Okochi M., Usami M.,
RA Shirasawa T., Mori H.;
RT "Identification and characterization of presentin I-467, I-463 and
RT I-374.";
RL FEBS Lett. 381:7-11(1996).
[3]
RN SEQUENCE FROM N.A.
RP Rowen L., Madan A., Qin S., Abbasi N., Dors M., Ratcliffe A.,
RA Madan A., Dickhoff R., Shaffer T., James R., Lasky S., Hood L.;
RT "Complete sequence of the gene for presentin I.";
RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
[4]
RN SEQUENCE OF 1-113 FROM N.A.
RP Tsujimura A., Hashimoto-Gotoh T.;
RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
[5]
RN SUPRACELLULAR LOCATION, AND TISSUE SPECIFICITY.
RP MEDLINE=96160372; PubMed=8574969;
RX Kovacs D.M., Fausett H.J., Page K.J., Kim T.-W., Molr R.D.,
RA Merriam D.E., Hollister R.D., Hallmark O.G., Mancini R.,
RA Felsenstein K.M., Hyman B.T., Tanzi R.E., Masco W.;
RT "Alzheimer-associated presentins 1 and 2: neuronal expression in
RT brain and localization to intracellular membranes in mammalian
RT cells.";
RL Nat. Med. 2:224-229(1996).

RA [6]
 RP PROCESSING.
 RX MEDLINE-97317150; PubMed-9173929;
 RA Podlany M.B., Citron M., Amarante P., Sherrington R., Xia W.,
 RA Zhang J., Diehl T., Levesque G., Fraser P., Haas C., Koo E.H.,
 RA Seubert P., St George-Hyslop P., Teplow D.B., Selkoe D.J.;
 RT "Presenilin proteins undergo heterogeneous endoproteolysis between
 RT Thr291 and Ala299 and occur as stable N- and C-terminal fragments in
 RT normal and Alzheimer brain tissue.";
 RL Neurobiol. Dis. 3:325-337(1997).
 RN [7]
 RP FUNCTION, AND MUTAGENESIS OF MET-292.
 RX MEDLINE-20014554; PubMed-10545183;
 RA Steiner H., Romig H., Pesold B., Philipp U., Baader M., Citron M.,
 RA Loetscher H., Jacobsen H., Haas C.;
 RT "Amyloidogenic function of the Alzheimer's disease-associated
 RT presenilin 1 in the absence of endoproteolysis.";
 RL Biochemistry 38:14600-14605(1999).
 RN [8]
 RP FUNCTION.
 RX MEDLINE-20062913; PubMed-10593990;
 RA Ray W.J., Yao M., Munn J., Schroeter E.H., Safiy P., Wolfe M.,
 RA Selkoe D.J., Kopan R., Goate A.M.;
 RT "Cell surface presenilin-1 participates in the gamma-secretase-like
 RT proteolysis of Notch.";
 RL J. Biol. Chem. 274:36801-36807(1999).
 RN [9]
 RP FUNCTION, AND MUTAGENESIS OF ASP-257 AND ASP-385.
 RX MEDLINE-99221485; PubMed-10206644;
 RA Wolfe M.S., Xia W., Ostaszewski B.L., Diehl T.S., Kimberly W.T.,
 RA Selkoe D.J.;
 RT "Two transmembrane aspartates in presenilin-1 required for presenilin
 RT endoproteolysis and gamma-secretase activity.";
 RL Nature 398:513-517(1999).
 RN [10]
 RP FUNCTION, AND MUTAGENESIS OF ASP-257 AND ASP-385.
 RX MEDLINE-20359495; PubMed-10899933;
 RA Bereznova O., Jack C., McLean P., Aster J.C., Hicks C., Xia W.,
 RA Wolfe M.S., Kimberly W.T., Weinmaster G., Selkoe D.J., Hyman B.T.;
 RT "Aspartate mutations in presenilin and gamma-secretase inhibitors both
 RT impair notch proteolysis and nuclear translocation with relative
 RT preservation of notch signaling.";
 RL J. Neurochem. 75:583-593(2000).
 RN [11]
 RP FUNCTION, AND MUTAGENESIS OF LEU-286.
 RX MEDLINE-20283925; PubMed-10811883;
 RA Kulic L., Walter J., Multhaup G., Teplow D.B., Baumeister R.,
 RA Romig H., Capell A., Steiner H., Haas C.;
 RT "Separation of presenilin function in amyloid beta-peptide generation
 RT and endoproteolysis of Notch.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:5913-5918(2000).
 RN [12]
 RP FUNCTION.
 RX PubMed-11226248;
 RA Bakl L., Marandaud P., Efthimiopoulos S., Georgakopoulos A., Wen P.,
 RA Cui W., Shioi J., Koo E., Ozawa M., Friedrich V.L., Robakis N.K.;
 RT "Presenilin-1 binds cytoplasmic epithelial cadherin, inhibits
 RT cadherin/p120 association, and regulates stability and function of
 RT the cadherin/catenin adhesion complex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:2381-2386(2001).
 RN [13]
 RP INTERACTION WITH DELTA-2 CATENIN.
 RX MEDLINE-99155075; PubMed-10037471;
 RA Levesque G., Yu G., Nishimura M., Zhang D.M., Levesque L., Yu H.,
 RA Xu D., Liang Y., Rogeave E., Ikeda M., Murgolo N., Wang L.,
 RA Vandervere P., Bayne M.L., Strader C.D., Rommens J.M., Fraser P.E.,
 RA St George-Hyslop P.;
 RT "Presenilins interact with armadillo proteins including
 RT neural-specific plakophilin-related protein and beta-catenin.";
 RL J. Neurochem. 72:999-1008(1999).
 RN [14]
 RP REVIEW ON VARIANTS.
 RX MEDLINE-97029239; PubMed-8875251;
 RA Cruts M., Hendriks L., Van Broeckhoven C.;
 RT "The presenilin genes: a new gene family involved in Alzheimer disease
 RT pathology.";
 RL Hum. Mol. Genet. 5:1449-1455(1996).
 RN [15]
 RP REVIEW ON VARIANTS.
 RX MEDLINE-98180715; PubMed-9521418;
 RA Cruts M., van Broeckhoven C.;
 RT "Presenilin mutations in Alzheimer's disease.";
 RL Hum. Mutat. 11:183-190(1998).
 RN [16]
 RP VARIANTS AD THR-143 AND ALA-384.
 RX MEDLINE-9617673; PubMed-8634711;
 RA Cruts M., Backhovens H., Wang S.-Y., van Gaasen G., Theuns J.,
 RA de Jonghe C., Wehnert A., de Voacht J., de Winter G., Cras P.,
 RA Bruylant M., Datsen N., Weissenbach J., den Dunnen J.T., Martin J.-J.,
 RA Hendriks L., Van Broeckhoven C.;
 RT "Molecular genetic analysis of familial early-onset Alzheimer's
 RT disease linked to chromosome 14q24.3.";
 RL Hum. Mol. Genet. 4:2363-2372(1995).
 RN [17]
 RP VARIANTS AD L-82; H-115; T-139; R-163; T-231; L-264; V-392 AND Y-410.
 RX MEDLINE-9617674; PubMed-8634712;
 RA Campion D., Flaman J.-M., Brice A., Haneguin D., Dubois B.,
 RA Martin C., Moreau V., Charbonnier F., Didierjean O., Tardieu S.,
 RA Penet C., Puel M., Pasquier F., le Doze F., Bellis G., Calenda A.,
 RA Hellig R., Martinez M., Mallet J., Bellis M., Clerget-Darpoux F.,
 RA Agid Y., Frebourg T.;
 RT "Mutations of the presenilin 1 gene in families with early-onset
 RT Alzheimer's disease.";
 RL Hum. Mol. Genet. 4:2373-2377(1995).
 RN [18]
 RP VARIANTS AD VAL-260; VAL-285 AND VAL-392.
 RX MEDLINE-95379971; PubMed-7651536;
 RA Rogeev E.I., Sherrington R., Rogaeva E.A., Levesque G., Ikeda M.,
 RA Liang Y., Chi H., Lin C., Holman K., Tsuda T., Mar L., Sorbi S.,
 RA Nachnas B., Placentini S., Amaducci L., Chumakov I., Cohen D.,
 RA Lannfelt L., Fraser P.E., Rommens J.M., St George-Hyslop P.H.;
 RT "Familial Alzheimer's disease in kindreds with missense mutations in
 RT a gene on chromosome 1 related to the Alzheimer's disease type 3
 RT gene.";
 RL Nature 376:775-778(1995).
 RN [19]
 RP VARIANTS AD V-139; V-146; Y-163; T-267; A-280 AND G-280.
 RX MEDLINE-96024664; PubMed-7550356;
 RA Clark R.F., Hutton M., Fuldner R.A., Froelich S., Karran E.,
 RA Talbot C., Crook R., London C.L., Prihar G., He C., Korenblatt K.,
 RA Martinez A., Wragg M., Busfield F., Behrens M.I., Myers A., Norton J.,
 RA Morris J., Mehta N., Pearson C., Lincoln S., Baker M., Duff K.,
 RA Zehr C., Perez-Tur J., Houlden H., Rutz A., Ossa J., Lopera F.,
 RA Arcos M., Madrigal L., Collinge J., Humphreys C., Asworth T.,
 RA Sarter S., Fox N.C., Harvey R., Kennedy A., Rogge P.R., Cliffe R.T.,
 RA Phillips C.A., Venter J.C., Forsell L., Axelman K., Lilius L.,
 RA Johnston J., Cowburn R., Viitanen M., Winblad B., Kosik R.S.,
 RA Haltia M., Poyhonen M., Dickson D., Mann D., Neary D., Snowden J.,
 RA Lantos P., Lannfelt L., Rossor M.N., Roberts G.W., Adams M.D.,
 RA Hardy J., Goate A.M.;
 RT "The structure of the presenilin 1 (S182) gene and identification of
 RT six novel mutations in early onset AD families.";
 RL Nat. Genet. 11:219-222(1995).
 RN [20]
 RP VARIANTS AD PHE-96; ARG-163 AND THR-213.
 RX MEDLINE-96310408; PubMed-8733303;
 RA Kamano K., Sato S., Sakaki Y., Yoshikawa A., Nishiwaki Y., Takeda H.,
 RA Tanabe H., Nishimura T., Li K., St George-Hyslop P.H., Miki T.,
 RA Ogihara T.;
 RT "Three different mutations of presenilin 1 gene in early-onset
 RT Alzheimer's disease families.";
 RL Neurosci. Lett. 208:195-198(1996).
 RN [21]
 RP VARIANT AD ASP-135.
 RX MEDLINE-97369208; PubMed-9225696;
 RA Crook R., Ellis R., Shanks M., Thal L.J., Perez-Tur J., Baker M.,

Query Match 99.8%; Score 2387; DB 1; Length 467;
Best Local Similarity 99.8%; Pred. No. 1,4e-150;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNLSTNVRSONDRERQHNDRSLGHPPLSGRPGNSR 60
DB 1 MTELPAPLSYFQNAQMSDNLSTNVRSONDRERQHNDRSLGHPPLSGRPGNSR 60
QY 61 OVEDEDEDEDELTKYAKAHVIMLFVVTLCMYYVATISVSFTYTKDGLITPTPE 120
DB 61 QVEDEDEDEDELTKYAKAHVIMLFVVTLCMYYVATISVSFTYTKDGLITPTPE 120
QY 121 DTEYVGOALSHLNAAMISIVYMTLLVLYRCYKVIHMLISSLILFFFSFI 180
DB 121 DTEYVGOALSHLNAAMISIVYMTLLVLYRCYKVIHMLISSLILFFFSFI 180
QY 181 YLGEVFKTYNAVDYITVALLIMNGVGMISIHKGPLRQOAYLIMISALMALVFTKY 240
DB 181 YLGEVFKTYNAVDYITVALLIMNGVGMISIHKGPLRQOAYLIMISALMALVFTKY 240
QY 241 LPEWTAMILAVISYVDLVAVLCPRGLRMVETAOERNETLFPALISSYTWMLVNAE 300
DB 241 LPEWTAMILAVISYVDLVAVLCPRGLRMVETAOERNETLFPALISSYTWMLVNAE 300
QY 301 GDPEAQRVSKSKYNAESTERESODTYAENDGSEMEAOQRSHLGPHRSTPESRAA 360
DB 301 GDPEAQRVSKSKYNAESTERESODTYAENDGSEMEAOQRSHLGPHRSTPESRAA 360
QY 361 VOELSSSILAGEDPERGVKLGDFIFYSVLVGKASATASGDMWTJTACFAVAILIGLCL 420
DB 361 VOELSSSILAGEDPERGVKLGDFIFYSVLVGKASATASGDMWTJTACFAVAILIGLCL 420
QY 421 TLLLLAIFKKALPALPISITFGVFFYFATDYLVOPFMDLAFHORYI 467
DB 421 TLLLLAIFKKALPALPISITFGVFFYFATDYLVOPFMDLAFHORYI 467

RESULT 2
PSNL_MTCMU STANDARD; PRT: 467 AA.
ID PSNL_MTCMU P79802;
AC 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Presentin 1 (PS-1).
GN PSNL OR PSNL1 OR PS1.
OS Microcebus murinus (Lesser mouse lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Chelirogaletidae;
OC Microcebus.
OX NCBI_TaxID=30608;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97079199; PubMed=8920931;
RA Calenda A., Mestre-Frances N., Czech C., Pradler L., Bons N.,
RA Bellis M.;
RT "Molecular cloning, sequencing, and brain expression of the
RT presentin 1 gene in Microcebus murinus.";
RL Blochem. Biophys. Res. Commun. 228:430-439(1996).
CC -1- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
CC EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE.
CC MAY FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS.
CC -1- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTE) AND A
CC C-TERMINAL (CTE) ENDOPROTEOLYTICAL FRAGMENT (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC ENDOPASMIC RETICULUM (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: I-467 (SHOWN HERE) AND I-
CC 463; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: FOUND PREDOMINANTLY IN NEURONS OF THE
CC DIFFERENT CORTICAL LAYERS AND HIPPOCAMPUS BUT ALSO IN SUBCORTICAL
CC STRUCTURES.

CC -1- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PRESENTIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
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DR EMBL: 271333; CA95930.1; -
DR MEROPS: A22.001; -
DR InterPro: IPR001108; Presentin.
DR Pfam: PF01080; Presentin; 1.
DR PRINTS: PR01072; PRESENTIN.
KW Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack;
KW Alternative splicing.
FT CHAIN 1 298 PRESENTIN 1 NTE SUBUNIT (BY SIMILARITY).
FT DOMAIN 1 81 PRESENTIN 1 CTE SUBUNIT (BY SIMILARITY).
FT TRANSSEM 82 102 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 103 132 LUMENAL (POTENTIAL).
FT TRANSSEM 133 153 POTENTIAL.
FT DOMAIN 154 160 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 161 181 POTENTIAL.
FT DOMAIN 182 190 LUMENAL (POTENTIAL).
FT TRANSSEM 191 211 POTENTIAL.
FT DOMAIN 212 220 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 221 241 LUMENAL (POTENTIAL).
FT DOMAIN 242 243 POTENTIAL.
FT TRANSSEM 244 264 LUMENAL (POTENTIAL).
FT DOMAIN 265 407 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 408 428 POTENTIAL.
FT TRANSSEM 433 453 POTENTIAL.
FT SITE 291 292 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY
FT SIMILARITY).
FT SITE 292 293 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY
FT SIMILARITY).
FT VARSPIC 26 29 MISSING (IN ISOFORM I-463).
FT SEQUENCE 467 AA; 52384 MW; D986FF2CA7F2975C CRC64;
SO
Query Match 95.1%; Score 2275; DB 1; Length 467;
Best Local Similarity 94.9%; Pred. No. 3.5e-143;
Matches 443; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNLSTNVRSONDRERQHNDRSLGHPPLSGRPGNSR 60
DB 1 MTELPAPLSYFQNAQMSDNLSTNVRSONDRERQHNDRSLGHPPLSGRPGNSR 60
QY 61 OVEDEDEDEDELTKYAKAHVIMLFVVTLCMYYVATISVSFTYTKDGLITPTPE 120
DB 61 PVERDEDEDEDELTKYAKAHVIMLFVVTLCMYYVATISVSFTYTKDGLITPTPE 120
QY 121 DTEYVGOALSHLNAAMISIVYMTLLVLYRCYKVIHMLISSLILFFFSFI 180
DB 121 DTEYVGOALSHLNAAMISIVYMTLLVLYRCYKVIHMLISSLILFFFSFI 180
QY 181 YLGEVFKTYNAVDYITVALLIMNGVGMISIHKGPLRQOAYLIMISALMALVFTKY 240
DB 181 YLGEVFKTYNAVDYITVALLIMNGVGMISIHKGPLRQOAYLIMISALMALVFTKY 240
QY 241 LPEWTAMILAVISYVDLVAVLCPRGLRMVETAOERNETLFPALISSYTWMLVNAE 300
DB 241 LPEWTAMILAVISYVDLVAVLCPRGLRMVETAOERNETLFPALISSYTWMLVNAE 300
QY 301 GDPEAQRVSKSKYNAESTERESODTYAENDGSEMEAOQRSHLGPHRSTPESRAA 360
DB 301 GDPEAQRVSKSKYNAESTERESODTYAENDGSEMEAOQRSHLGPHRSTPESRAA 360
QY 361 VOELSSSILAGEDPERGVKLGDFIFYSVLVGKASATASGDMWTJTACFAVAILIGLCL 420
DB 361 VOELSSSILAGEDPERGVKLGDFIFYSVLVGKASATASGDMWTJTACFAVAILIGLCL 420

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Presentin 1 (PS-1) (S182 protein).
GN PSEN1 OR PSEN1.
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=9719371; PubMed=9047347;
RA Taniguchi T., Hashimoto T., Taniguchi R., Shimada K., Kawamata T.,
RA Yaoda M., Nakai M., Terashima A., Koizumi T., Maeda K., Tanaka C.;
RT "Cloning of the cDNA encoding rat presentin-1.";
RL Gene 186:73-75(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=9625262; PubMed=8710164;
RA Takahashi H., Mureyama M., Takashima A., Mercken M., Nakazato Y.,
RA Noguchi K., Imahori K.;
RT "Molecular cloning and expression of the rat homologue of
RT presentin-1.";
RL Neurosci. Lett. 206:113-116(1996).
CC -1- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
CC EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE.
CC MAY FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS.
CC -1- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A
CC C-TERMINAL (CTF) ENDOPROTEOLYTICAL FRAGMENT (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND A
CC ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- PM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PRESENTIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D82578; BAA1575.1; -;
DR EMBL: D82363; BAA1564.1; -;
DR MEROPS: A22.001; -;
DR InterPro: IPR001106; Presentin.
DR Pfam: PF01080; Presentin.1.
DR PRINTS: PRO1072; PRESENTIN.
KW Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack.
FT CHAIN 1 298 PRESENTIN 1 NTF SUBUNIT (BY SIMILARITY).
FT CHAIN 299 468 PRESENTIN 1 CTF SUBUNIT (BY SIMILARITY).
FT DOMAIN 1 82 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 83 103 POTENTIAL.
FT DOMAIN 104 132 LUMENAL (POTENTIAL).
FT TRANSMEM 133 153 POTENTIAL.
FT DOMAIN 154 160 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 161 181 POTENTIAL.
FT DOMAIN 182 194 LUMENAL (POTENTIAL).
FT TRANSMEM 195 215 POTENTIAL.
FT DOMAIN 216 220 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 221 241 POTENTIAL.
FT DOMAIN 242 243 LUMENAL (POTENTIAL).
FT TRANSMEM 244 264 POTENTIAL.
FT DOMAIN 265 407 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 408 428 POTENTIAL.
FT TRANSMEM 433 453 POTENTIAL.
FT SITE 291 292 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY
FT SIMILARITY).
FT SITE 292 293 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY
FT SIMILARITY).
FT SITE 293 293 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY
FT SIMILARITY).
FT CONFLICT 234 234 A -> S (IN REF. 2).
FT CONFLICT 381 381 K -> R (IN REF. 2).
SQ SEQUENCE 468 AA; 52790 MW; 17CB791EB88A16FC0 CRC64;

Query Match 92.4%; Score 2209.5; DB 1; Length 468;
Best Local Similarity 92.1%; Pred. No. 7.3e-139;
Matches 432; Conservative 19; Mismatches 15; Indels 3; Gaps 3;
QY 1 MTELPAPLSTPQNAQMSDESNHLSNVSQNDNRQEHNRSLGHPPLNSGRQGN-S 59
DB 1 MTEIPAPLSTPQNAQMSDSH-SSSVSRQNDNQEHQHDRQLNDPESISGRQSNFT 59
QY 60 RQVVEQDEDEDELTKYGAHVIMLVFVPTLCMVVVVATIKSVSFYRKDGQIYTPPT 119
DB 60 RQVVEQDEDEDELTKYGAHVIMLVFVPTLCMVVVVATIKSVSFYRKDGQIYTPPT 119
QY 120 EDTFVGRALHSLTNAIMISVIVMTLLVLLVLYKRCYKIHAWLIISSLLFFPSF 179
DB 120 EDTFVGRALHSLTNAIMISVIVMTLLVLLVLYKRCYKIHAWLIISSLLFFPSF 179
QY 180 IYLGVEFTYVAVDYITVALLINMLGVGMISIMKSPRLQQAVALIMISALMLVPIK 239
DB 180 IYLGVEFTYVAVDYITVALLINMLGVGMISIMKSPRLQQAVALIMISALMLVPIK 239
QY 240 YLPETAMLLIAVISVYDLVAVLCPEKPLRLVETAOERNEFLPALIYSSTMVLVMA 299
DB 240 YLPETAMLLIAVISVYDLVAVLCPEKPLRLVETAOERNEFLPALIYSSTMVLVMA 299
QY 300 EGDPEAORVRVSKSVYNAESPTER-ESODTYAENDDGFSEEAQRDSHLGPHRSTPSR 358
DB 300 EGDPEAORVRVSKSVYNAESPTER-ESODTYAENDDGFSEEAQRDSHLGPHRSTPSR 358
QY 359 AAVQELSSIIAGDEPBERGVKLGIDETIFYSVLVKKSAFASGDMNTTIAFVAIILGL 418
DB 359 AAVQELSSIIAGDEPBERGVKLGIDETIFYSVLVKKSAFASGDMNTTIAFVAIILGL 418
QY 419 CTTLLLAIFKKALPALPILSTFGLVFFPADDYLVQPPMDLAFHQFI 467
DB 420 CTTLLLAIFKKALPALPILSTFGLVFFPADDYLVQPPMDLAFHQFI 467

RESULT 5
PSN1_BOVIN STANDARD; PRT; 478 AA.
AC Q9XT97;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Presentin 1 (PS-1).
GN PSEN1.
OS Bos taurus (Bovine).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Sahara N., Shirasawa T., Mori H.;
RT "Molecular cloning of bovine presentin 1 gene.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
CC EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE. MAY
CC FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS (BY
CC SIMILARITY).
CC -1- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A
CC C-TERMINAL (CTF) ENDOPROTEOLYTICAL FRAGMENT (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- PM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PRESENTIN FAMILY.
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[illegible]

AC	012976;	Rel. 38, Created)
DT	15-JUL-1999	(Rel. 38, Last sequence update)
DT	15-JUL-1999	(Rel. 38, Last annotation update)
DT	15-JUL-1999	(Rel. 38, Last annotation update)
DE	Presentinlin alpha.	
GN	PS-ALPHA.	
OS	Xenopus laevis (African clawed frog).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;	
OC	Xenopodinae; Xenopus.	
OX	NCBI_TaxID=8355;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Brain.	
RX	MEDLINE=97223465; PubMed=9070286;	
RA	Tsujimura A., Yasojima K., Hashimoto-Gotoh T.;	
RT	"Cloning of Xenopus presentinlin alpha and -beta cDNAs and their	
RT	differential expression in oogenesis and embryogenesis.";	
RL	Biochem. Biophys. Res. Commun. 231:392-396(1997).	
CC	-1- FUNCTION: MAY PLAY A ROLE IN NEGATIVE REGULATION OF APOPTOTIC	
CC	CASCADES DURING OOGENESIS AND EMBRYOGENESIS, AND IN	
CC	DEVELOPMENTALLY MATURED TISSUES SUCH AS BRAIN TISSUE.	
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).	
CC	-1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN OVARIES AND TO A LESSER	
CC	EXTENT IN TESTIS, INTESTINE, KIDNEY, BRAIN, EYE AND LUNG. WEAK	
CC	EXPRESSION IN LIVER AND HEART. PRESENT IN TRACE AMOUNTS IN	
CC	SKELETAL MUSCLE.	
CC	-1- DEVELOPMENTAL STAGE: ABUNDANT IN EARLY STAGES OF OOGENESIS. THE	
CC	EXPRESSION IS RAPIDLY REDUCED BETWEEN MEIOTIC MATURATION AND	
CC	FERTILIZATION STAGES.	
CC	-1- SIMILARITY: BELONGS TO THE PRESENTINLIN FAMILY.	
CC	-----	
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; D84427; BAA19570.1; -.	
DR	MEROPS; A22.001; -.	
DR	InterPro: IPR001108; Presentinlin.	
DR	Pfam; PF01080; Presentinlin; 1.	
DR	PRINTS; PRO1072; PRESENTINLIN.	
KW	transmembrane; Glycoprotein.	
FT	TRANSMEM 48 68	POTENTIAL.
FT	TRANSMEM 99 119	POTENTIAL.
FT	TRANSMEM 127 147	POTENTIAL.
FT	TRANSMEM 161 181	POTENTIAL.
FT	TRANSMEM 184 204	POTENTIAL.
FT	TRANSMEM 210 230	POTENTIAL.
FT	TRANSMEM 247 267	POTENTIAL.
FT	TRANSMEM 374 394	POTENTIAL.
FT	TRANSMEM 399 419	POTENTIAL.
FT	CARBOHYD 245 245	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 371 371	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE 433 AA; 48301 MW; 71CCEB3F6BB9C0AF CRC64;	
Query Match	75.4%; Score 1804; DB 1; Length 433;	
Best Local Similarity	83.0%; Pred. No. 3.8e-112;	
Matches 357; Conservative 27; Mismatches 44; Indels 2; Gaps 2;		
OY	39 NDRSLGHPRLSLNGPGRGNSQVVEODEDEDELTLTKYGAHVIMLVPVTLCAVVVA 98	
DB	5 SERRNENSESOQNOQTOSSQVLEODEDEDELTLTKYGAHVIMLVPVTLCAVVVA 64	
OY	99 TIKSVSYTRKDGQILYPTFEDTETVGOALSHLSILNAAMISVIVMTILLVLYKYRC 158	
DB	65 TIKSVSYTRKDGQILYPTFEDTETVGOALSHLSILNAAMISVIVMTILLVLYKYRC 124	
OY	159 KYVHAMLIISSLLIFFSFYLYGLGVKRTNVANDITYVALIINLGVGMISHHMGP 218	

Db 125 YKVIHGLWIISSLLLLFFFSYIYIGCEVEKTYNVAVDYITLLALLINFGVGMICIHMKGP 184
Oy 219 LRLOQAVLIMISALMALVFIKYPMTWLIAVTSYDIAVLGCPKPLMLVETAOER 278
Db 185 LLLQOAVLIMISALMALVFIKYPMTWLIAVTSYDIAVLGCPKPLMLVETAOER 244
Oy 279 NETLEPALIYSTWMLVMAEGDEPEAOORYSKNSKYNAES-TERESODTVAENDGGFS 337
Db 245 NETLEPALIYSTWMLVMAEGDEPEAOORYSKNSKYNAES-TERESODTVAENDGGFS 303
Oy 338 EEMEQORSHLGPFRSTESRAVAOELSSILAGEDEPERGVKGLGDFIFYSVLVGRAS 397
Db 304 TTMEPRNAOIGPINSPESESRVAOALPSNPSPEDEPERGVKGLGDFIFYSVLVGRAS 363
Oy 398 ATASGDMWTTIACFAVAILIGLCTLLLAIFKKAIPALPISITGTLVYFPAVDYVOPFM 457
Db 364 ATASGDMWTTIACFAVAILIGLCTLLLAIFKKAIPALPISITGTLVYFPAVDYVOPFM 423
Oy 458 DOLAHEQFYI 467
Db 424 DOLAHEQFYI 433
RESULT 7
PSN2_HUMAN
ID PSN2_HUMAN STANDARD: PRT: 448 AA.
AC P49810:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Presenilin 2 (PS-2) (STM-2) (E5-1) (AD3LP) (AD5).
GN PSN2 OR PSN2 OR AD4 OR PS2 OR STM2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A., AND VARIANT FAD ILE-141.
RA MEDLINE=95365816; PubMed=7638622;
RA Levy-Lahad E., Masco W., Poorkaj P., Romano D.M., Oshima J.,
RA Pettingell W.H., Yu C.-E., Jondro P.D., Schmidt S.D., Wang K.,
RA Crowley A.C., Fu Y.-H., Guenette S.Y., Galas D., Nemens E.,
RA Wajsbom E.M., Bird T.D., Schellenberg G.D., Tanzi R.E.;
RT "Candidate gene for the chromosome 1 familial Alzheimer's disease
RT locus.";
RT Science 269:973-977(1995).
RL [2]
RN SEQUENCE FROM N.A., AND VARIANTS FAD ILE-141 AND VAL-239.
RP TISSUE=Brain, and Colon;
RC MEDLINE=95379971; PubMed=7651536;
RA Rogeev E.I., Sherrington R., Rogeeva E.A., Levesque G., Ikeda M.,
RA Liang Y., Chi H., Lin C., Holman K., Tsuda T., Mar L., Sorbi S.,
RA Nacmias B., Placentini S., Maducl L., Chumakov I., Cohen D.,
RA Lannfelt L., Fraser P.E., Rommens J.M., St George-Hyslop P.H.;
RT "Familial Alzheimer's disease in kindreds with missense mutations in
RT a gene on chromosome 1 related to the Alzheimer's disease type 3
RT gene.";
RT Nature 376:775-778(1995).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=96109229; PubMed=8618867;
RA Li J., Ma J., Potter H.;
RT "Identification and expression analysis of a potential familial
RT Alzheimer disease gene on chromosome 1 related to AD.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:12180-12184(1995).
RN [4]
RN SEQUENCE FROM N.A.
RA Levy-Lahad E., Poorkaj P., Wang K., Fu Y.H., Oshima J.,
RA Mulligan J., Schellenberg G.D.;
RT Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RX SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
MEDLINE=96160372; PubMed=8574969;

RA Kovacs D.M., Fausett H.J., Page K.J., Kim T.-W., Moir R.D.,
RA Merriam D.E., Hollister R.D., Hallmark O.G., Mancini R.,
RA Feisenstein K.M., Hyman B.T., Tanzi R.E., Masco W.;
RT "Alzheimer-associated presenilins 1 and 2: neuronal expression in
RT brain and localization to intracellular membranes in mammalian
RT cells.";
RL Nat. Med. 2:224-229(1996).
RN [6]
RN MUTAGENESIS OF ASP-366.
RP MEDLINE=99428546; PubMed=10497236;
RA Steiner H., Duff K., Capell A., Romig H., Grim M.G., Lincoln S.,
RA Hardy J., Yu X., Picciano M., Fichtelner K., Clifton M., Kopan R.,
RA Pezold B., Keck S., Baader M., Tomita T., Iwatsubo T., Baumeister R.,
RA Haas C.;
RT "A loss of function mutation of presenilin-2 interferes with amyloid
RT beta-peptide production and notch signaling.";
RL J. Biol. Chem. 274:28669-28673(1999).
RN [7]
RN MUTAGENESIS OF ASP-263 AND ASP-366.
RP MEDLINE=20119269; PubMed=10652302;
RA Kimberly W.T., Xia W., Rahmati T., Wolfe M.S., Selkoe D.J.;
RT "The transmembrane aspartates in presenilin 1 and 2 are obligatory for
RT gamma-secretase activity and amyloid beta-protein generation.";
RL J. Biol. Chem. 275:3173-3178(2000).
RN [8]
RN REVIEW ON VARIANTS.
RP MEDLINE=98180715; PubMed=9521418;
RA Cruts M., van Broeckhoven C.;
RT "Presenilin mutations in Alzheimer's disease.";
RL Hum. Mutat. 11:183-190(1998).
RN [9]
RN VARIANT AD HIS-62.
RP MEDLINE=98046005; PubMed=9384602;
RA Cruts M., van Duyn C.M., Backhovens H., van den Broeck M.,
RA Weinert A., Serneels S., Sherrington R., Hutton M., Hardy J.,
RA St George-Hyslop P.H., Hofman A., van Broeckhoven C.;
RT "Estimation of the genetic contribution of presenilin-1 and -2
RT mutations in a population-based study of presenile Alzheimer
RT disease.";
RL Hum. Mol. Genet. 7:43-51(1998).
RN [10]
RN VARIANT AD ILE-148.
RA Lao J.I., Beyer K., Fernandez-Novoa L., Cacabelos R.;
RT "A novel mutation in the predicted TM2 domain of the presenilin 2 gene
RT in Spanish patient with late-onset Alzheimer's disease.";
RL Neurogenetics 1:293-296(1998).
RN [11]
RN VARIANTS EOAD PRO-122 AND ILE-239.
RP MEDLINE=20100613; PubMed=10631141;
RA Finch U., Mueller-Thomsen T., Mann U., Eggers C., Marksteiner J.,
RA Meins W., Bihetti G., Alberici A., Hock C., Nitsch R.M., Gal A.;
RT "High prevalence of pathogenic mutations in patients with early-onset
RT dementia detected by sequence analyses of four different genes.";
RL Am. J. Hum. Genet. 66:110-117(2000).
CC -1- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
CC EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE. MAY
CC FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS. IS INVOLVED
CC IN THE PROTEOLYTIC PROCESSING OF AMYLOID PRECURSOR PROTEIN (APP)
CC AND OF NOTCH1.
CC -1- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A
CC C-TERMINAL (CTF) ENDOPROTEOLYTIC FRAGMENT. ASSOCIATES WITH
CC NICASTRIN AND WITH PROTEOLYTIC PROCESSED C-TERMINAL FRAGMENTS C83
CC AND C99 OF THE AMYLOID PRECURSOR PROTEIN (APP).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC ENDOPLASMIC RETICULUM.
CC -1- TISSUE SPECIFICITY: THE LARGER FORM IS SEEN IN THE PLACENTA,
CC SKELETAL MUSCLE AND HEART WHILE THE SHORTER FORM IS SEEN IN THE
CC HEART, BRAIN, PLACENTA, LIVER, SKELETAL MUSCLE AND KIDNEY.
CC -1- PTM: HETEROGENEOUS PROTEOLYTIC PROCESSING GENERATES N-TERMINAL
CC AND C-TERMINAL FRAGMENTS.
CC -1- PTM: PHOSPHORYLATED ON SERINE RESIDUES.
CC -1- DISEASE: DEFECTS IN PSN2 ARE RESPONSIBLE FOR EARLY-ONSET
CC AUTOSOMAL DOMINANT ALZHEIMER DISEASE (ROAD), WHICH IS THE MOST

SEVERE FORM OF THE DISEASE. COMPLETE PENETRANCE, AN ONSET OCCURRING AS EARLY AS 30 YEARS OF AGE. THE SECOND FORM IS LATE-ONSET (LOAD) ALSO CALLED THE FAMILIAL ALZHEIMER DISEASE (FAD). AD IS A NEURODEGENERATIVE DISORDER CHARACTERIZED BY PROGRESSIVE DEMENTIA, PARKINSONISM, AND DEPOSITION OF FIBRILLAR AMYLOID PROTEINS AS INTRANERONAL NEUROFIBRILLARY TANGLES, EXTRACELLULAR AMYLOID PLAQUES AND VASCULAR AMYLOID DEPOSITS.

-1- DISEASE: THREE CAUSATIVE GENES HAVE BEEN IDENTIFIED THAT WHEN MUTATED LEAD TO PRESENILE ALZHEIMER'S DISEASE: APP (AMYLOID PRECURSOR PROTEIN GENE), PSEN1 AND PSEN2. THESE THREE GENES ACCOUNT FOR HALF OF THE FAMILIES WITH AUTOSOMAL DOMINANT PRESENILE AD, WHICH REPRESENT APPROXIMATELY 10% OF THE WHOLE AD POPULATION. IN ADDITION, APOLIPOPROTEIN E HAS BEEN IDENTIFIED AS A RISK-MODIFYING LOCUS.

-1- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.

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CC

DR EMBL: L43964; AAB59557.1; -

DR EMBL: L44577; AAC42012.1; -

DR EMBL: U34349; AAC50290.1; -

DR EMBL: U50871; AAB50054.1; -

DR MEROPS: A22.002; -

DR Genew: HGNC:9509; PSEN2.

DR MIM: 600759; -

DR InterPro: IPR001108; Presenilin.

DR Pfam: PF01080; Presenilin; 1.

DR PRINTS: PR01072; PRESENILIN.

KW Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack; Alzheimer's disease; Disease mutation; Alternative splicing.

FT CHAIN 1 297

FT DOMAIN 1 87

FT TRANSMEM 88 108

FT DOMAIN 109 138

FT TRANSMEM 139 159

FT DOMAIN 160 166

FT TRANSMEM 167 187

FT DOMAIN 188 200

FT TRANSMEM 201 221

FT DOMAIN 222 243

FT TRANSMEM 244 249

FT DOMAIN 250 270

FT TRANSMEM 271 388

FT TRANSMEM 389 409

FT TRANSMEM 414 434

FT VARSPIC 263 296

FT VARIANT 62 62

FT VARIANT 122 122

FT VARIANT 141 141

FT VARIANT 148 148

FT VARIANT 239 239

FT VARIANT 239 239

FT MUTAGEN 263 263

FT MUTAGEN 366 366

FT CONFLICT 123 123

FT CONFLICT 325 325

FT CONFLICT 358 358 R -> SQG (IN REF. 3).

FT CONFLICT 432 448 NLVRFMDTLASHQLYI -> RKHSRFTQMN (IN REF. 3).

SO SEQUENCE 448 AA: 50140 MW: A927EEC623468116 CRC64;

Query Match 61.1%; Score 1461; DR 1; Length 448;

Best Local Similarity 65.5%; Pred. No. 1.7e-89;

Matches 305; Conservative 39; Mismatches 80; Indels 42; Gaps 8;

QY 3 ELPAFLPYQNMQMSQEDNLSVTSQNMNRROENRDR-SLGHPEPLSGRPOGNSHQ 61

DB 24 EEPTRSCQEGKQGPEDGNTQMSQENBEGDEDPKTVYSGVP-----GRPG----- 74

QY 62 VVEODEDEDELLTKGAKHVMLEFVPTLCMNVVATIKSVFTRKDGQILYPTPED 121

DB 75 -----LEELTLKYGAKHVMLEFVPTLCMNVVATIKSVFTRKDGQILYPTPED 127

QY 122 TETVQGRALHSLNMAIMSVYVMTLLVLYKRCYVTHAMLLISLLFFSFY 181

DB 128 TTSVQGRLLNSVNLMTIMSVYVMTFLVLYKRCYFHHGMLMSLLPLETYLY 187

QY 182 LGEVETVAVADYTYVALLINNLGVGMISIMKGPLRLOQAYLIMISALMAVFIKYL 241

DB 188 LGEVLTAVVADYPTLLTTLVNNFGAVGVCIMKGPLVLOQAYLIMISALMAVFIKYL 247

QY 242 PWTAMVLLIIVSYVDVAVLCRPGRLMVELTAQERNETLFPALYSSVTVVLYNMAEG 301

DB 248 PMSAMVILIGAIISYVDVAVLCRPGRLMVELTAQERNETLFPALYSSAMVTVGMATL 307

QY 302 DPEAQRRVSKNKYNASTERSQDPTVAENDDQGFSEEEAQRDSLGHRSPTESRAV 361

DB 308 DSSQCAL--QLPYDPE-MEEDSYDSFGF--PSTPEVEPLPTGPG----- 349

QY 362 QELSSIIAGDEPEERGVNLGLDFEFYSVLVYKASATASGDMNTTACFAVILGLCLT 421

DB 350 EEL-----EEBERGVNLGLGDFEFYSVLVYKAAATSGDMNTTACFAVILGLCLT 402

QY 422 LLLLAIFKALPALPILSTFTGVLFTFADYLVQPFMDQLAFHQFTI 467

DB 403 LLLLAIFKALPALPILSTFTGVLFTFADYLVQPFMDQLAFHQFTI 448

RESULT 8

PSN2_XENLA STANDARD; PRT; 449 AA.

ID PSN2_XENLA

AC 012877;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Presenilin beta.

GN PS-BETA.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RM (1)

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=97223465; PubMed=9070286;

RA Tsujimura A., Yasojima K., Hashimoto-Gotoh T.;

RT "Cloning of Xenopus presenilin-alpha and -beta cDNAs and their differential expression in oogenesis and embryogenesis.";

RL Biochem. Biophys. Res. Commun. 231:392-396(1997).

CC -1- FUNCTION: MAY PLAY A ROLE IN NEGATIVE REGULATION OF APOPTOTIC CASCADES DURING OOGENESIS AND EMBRYOGENESIS. AND IN DEVELOPMENTALLY MATURED TISSUES SUCH AS BRAIN TISSUE.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).

CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN OVARIES AND TO A LESSER EXTENT IN KIDNEY, BRAIN, EYE AND LUNG. WEAK EXPRESSION IN TESTIS, INTESTINE, LIVER AND HEART. PRESENT IN TRACE AMOUNTS IN SKELETAL MUSCLE.

CC -1- DEVELOPMENTAL STAGE: ABUNDANT IN EARLY STAGES OF OOOGENESIS AFTER

```

CC WHICH IT IS NEARLY CONSTANT.
CC -1- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
CC -----
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CC -----
CC EMBL: D84428; BAA19571.1; -.
CC MEROPS: A22.002; -.
CC InterPro: IPR001108; Presenilin.
CC Pfam: PF01080; Presenilin; 1.
CC DR PRINTS: PRO1072; PRESENILIN.
CC KW Transmembrane; glycoprotein.
CC FT TRANSMEM 92 112 POTENTIAL.
CC FT TRANSMEM 142 162 POTENTIAL.
CC FT TRANSMEM 170 190 POTENTIAL.
CC FT TRANSMEM 204 224 POTENTIAL.
CC FT TRANSMEM 227 247 POTENTIAL.
CC FT TRANSMEM 253 273 POTENTIAL.
CC FT TRANSMEM 291 311 POTENTIAL.
CC FT TRANSMEM 363 383 POTENTIAL.
CC FT TRANSMEM 390 410 POTENTIAL.
CC FT TRANSMEM 415 435 POTENTIAL.
CC FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 449 AA; 50274 MW; 2C2C105FC723F2B CnC64;
CC -----
OY Query Match 61.1%; Score 1460.5; DB 1; Length 449;
OY Best Local Similarity 63.9%; Pred. No. 1.8e-89;
OY Matches 301; Conservative 48; Mismatches 75; Indels 47; Gaps 7;
OY 2 TELPALSYFQNAQSCENHLSNTWRQSDNDRREHNDRLSGHPEPLSNRPG----- 57
DB 21 SESPLPLPYQDQVQASLEGLETSY-----HREKPPDSTONN---EDVPMGRISGADAY 69
OY 58 NSROYVEODEEDELTLKYGAKHVMLEFVPTLCMVVVVATIKSYSEYTRKDGLIYTP 117
DB 70 NSETTV---ENNEBELTLKYGARHYIMLFVPTLCMVVVVATIKSYSEYTRKDGLIYTP 126
OY 118 FTEDEETVGORALSHILNAAIMISYIVVTILVLVLYRYCKYVTHAMLIISLLFF 177
DB 127 FSEDSTVSGERLNSVLTLMISYILMTIFVLVLYRYCKYFTHGWLISLMLEFM 186
OY 178 SFYIYGEYFKYNNVVDITVALLIMNIGVYGMISIHKKGPRLQOAVLIMISALMAIYF 237
DB 187 TYIISEYFKYNNIMDPTLPMVIMNIGAVGIMTIHKKGPRLQOAVLIMISALMAIYF 246
OY 238 IKYLPENWAMLLIAYISYVDLVAVLCPPGPMLEVAETAOERNETLEPALIYSSTWMLVN 297
DB 247 IKYLPENWAMVILGAYISYVDLLAVLCPPGPMLEVAETAOERNETLEPALIYSSAMWYVG 306
OY 298 MAEGDEPEAKORYSKSKNAESTEREESODTYAENDDGGFSEBEAKORDSHLGPHRSTPS 357
DB 307 MAD-SATADGRMNQVOCHIDRNTPEGANSTV-----ED 338
OY 358 RAAVQELASSILAGBDP-EERGVYKGLGDDTFYSYLVGKASATASGDMNTTACVATILI 416
DB 339 AAEYRIQIQSNLSSDDPEERKVKYGLGDDTFYSYLVGKAAATASGDMNTTACVATILI 398
OY 417 GICLTLALLATFKKALPALPISITFGLEVYFATDVLVOPFMDQLAFHOFYI 467
DB 399 GICLTLALLAVFKKALPALPISITFGLEFYFSTDIIVRPMDTLASHQMYI 449

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DE 15-JUN-2002 (Rel. 41, last annotation update)
DR Presentinlin 2 (PS-2) (Fragment).
OS PSB2 OR PSNL2 OR PS2.
OC Microcebus murinus (lesser mouse lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Chirogaleidae;
OC Microcebus.
OX NCBI_TaxID=30608;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99167105; PubMed=10069575;
RA Calenda A., Mestre-Frances N., Czech C., Pradler L., Peter A.,
RA Petter M., Bons N., Bellis M.;
RT "Cloning of the presentinlin 2 cDNA and its distribution in brain of
RT the primate, Microcebus murinus: coexpression with betaAPP and Tau
RT proteins ";
RL Neurobiol. Dis. 5:333-333(1998).
CC -I- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
CC EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE. MAY
CC FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS (BY
CC SIMILARITY).
CC -I- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTE) AND A
CC C-TERMINAL (CTE) ENDOPROTEOLYTICAL FRAGMENT (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -I- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE PRESENTINLIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y10140; CAA7128.1; -.
DR MEROPS; A22.002; -.
DR InterPro; IPR001108; Presentinlin.
DR Pfam; PF01080; Presentinlin; 1.
DR PRINTS; PR01072; PRESENTINLIN.
KW Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack.
FT CHAIN 1 297 PRESENTINLIN 2 NTF SUBUNIT (BY SIMILARITY).
FT FT 298 445 PRESENTINLIN 2 CTF SUBUNIT (BY SIMILARITY).
FT DOMAIN 1 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 108 POTENTIAL.
FT DOMAIN 109 138 LUMENAL (POTENTIAL).
FT TRANSMEM 139 159 POTENTIAL.
FT DOMAIN 160 166 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 187 POTENTIAL.
FT DOMAIN 188 200 LUMENAL (POTENTIAL).
FT TRANSMEM 201 221 POTENTIAL.
FT DOMAIN 222 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 244 POTENTIAL.
FT DOMAIN 245 249 LUMENAL (POTENTIAL).
FT TRANSMEM 250 271 POTENTIAL.
FT DOMAIN 272 388 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 389 409 POTENTIAL.
FT TRANSMEM 414 434 POTENTIAL.
FT NON_TER 445 445
SQ SEQUENCE 445 AA; 49475 MW; 0A01A7646659E052 CRC64;

Query Match 60.6%; Score 1449; DB 1; Length 445;
Local Similarity 65.2%; Pred. No. 1e-88;
Matches 302; Conservative 41; Mismatches 78; Indels 42; Gaps 8;

QY 3 ELPAFLSYFQNAQMSQEDNHLSTNVSQNDNREORHNDNR-SLGHPEPLSNRGPGNSRQ 61
DB 24 ESPSPRSQEGGQGGEDGSDGTQWNRQIQSEEDGDDPDRYVSSGVP-----GRPG--- 74
QY 62 VEEQDEDEDELTLLTGAKHYMLEFVPVYTLCAVVVVATIKSVFTTRDKGLIITPFED 121

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Db 75 -----PEBELTKGAKHVMLSVPTLCMVVATKSKRFEYKNGQLYPTPTD 127
OY 122 TETVGORALHSILNAAIMISVIVMTLLVLYTKRYCYVIAHMLITSSLLFFPSFTY 181
    128 TPVSQRLNSVNTLIMISVIVMTIFLVLYTKRYCYFIHGMILMSSMLLFFFTY 187
Db 182 LGEVFTYVANDYITVALLINLVGMISIMHWKGPLRLOQAYLIMISALMAVFIKYL 241
    188 LGEVLTYYVANDYITVALLINLVGMISIMHWKGPLRLOQAYLIMISALMAVFIKYL 247
OY 242 PENTAMLLAVISVYDVLVLCRPGRLMVEAQRNRTIFPALYSSMFWLVMAAG 301
    248 PENSAMVILGALSVDLVAVLCRPGRLMVEAQRNRTIFPALYSSAMVTVMAKL 307
Db 302 DPEAQRVSKNSKYNAESTERESQDTVAENDDGFSEMEADQSHLGPFRSTPESRAV 361
    308 DPSSQAL--QLPYDPE-MEDSDYSLGE---PSYPEVEAPLPYGP----- 349
OY 362 QELSSSILAGEDEBERGVKLGDFIFYSVLYGKASATASGDMNTTACFVALIGLCT 421
    350 EEL-----EEBERGVKLGDFIFYSVLYGKAAATSGDMNTTACFVALIGLCT 402
OY 422 LLLAIFKKALPALPISITFGVFEFATDYLVQPFMDQLAFHQ 464
    403 LLLAIFKKALPALPISITFGVFEFATDYLVQPFMDQLAFHQ 445
Db 403 LLLAIFKKALPALPISITFGVFEFATDYLVQPFMDQLAFHQ 445

RESULT 10
PSN2_BOVIN STANDARD: PRT: 449 AA.
AC 09X96:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Presentin 2 (PS-2).
GN PSN2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Sahara N., Shirasawa T., Mori H.;
RT "Molecular cloning of bovine presentin 2 gene.";
RL Submitted (DEC-1997) to the EMBL/Genbank/CDJ databases.
CC -1- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
    EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE. MAY
    FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS (BY
    SIMILARITY).
CC -1- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTE) AND A
    C-TERMINAL (CTF) ENDOPEPTOLYTICAL FRAGMENT (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
    ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PRESENTIN FAMILY.
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    or send an email to license@isb-sb.ch).
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CC EMBL: AF038937; AAD39024.1; -.
DR MEROPS: A22.002; -.
DR InterPro: IPR001108; Presentin.
DR Pfam: PF01080; Presentin; 1.
DR PRINTS: PR01072; PRESENTIN.
KW Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack.
FT CHAIN 1 298 PRESENTIN 2 NTF SUBUNIT (BY SIMILARITY).

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FT CHAIN 299 449 PRESENTIN 2 CTF SUBUNIT (BY SIMILARITY).
FT DOMAIN 1 88 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 89 109 POTENTIAL.
FT DOMAIN 110 139 LUMENAL (POTENTIAL).
FT TRANSMEM 140 160 POTENTIAL.
FT DOMAIN 161 167 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 168 188 POTENTIAL.
FT DOMAIN 189 201 LUMENAL (POTENTIAL).
FT TRANSMEM 202 222 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 223 224 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 225 245 POTENTIAL.
FT DOMAIN 246 250 LUMENAL (POTENTIAL).
FT TRANSMEM 251 271 POTENTIAL.
FT DOMAIN 272 389 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 390 410 POTENTIAL.
FT TRANSMEM 415 435 POTENTIAL.
SQ SEQUENCE 449 AA: 50301 MW: 513500DaA2B2A7D CRC64:

Query Match 60.3%; Score 1441.5; DB 1; Length 449;
Best Local Similarity 64.3%; Pred. No. 3.3e-88;
Matches 299; Conservative 41; Mismatches 86; Indels 39; Gaps 7;

OY 3 ELPAPISTYQNMOMSEDNHLSNTRSONNREORHNDRSIGHPPLSNGRPGNSROY 62
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 24 EEPTRSCODRGLEDGESAQMWRQSEDEHEDDPRIYCGVP---GRPG----- 75
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
OY 63 VEODEEDELTLKYGAKHVMLEFVPTLCMVVATIKSVSFYRKDQLYPTPTEDT 122
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 76 -----LEEBELTKGAKHVMLEFVPTLCMVVATIKSVFTEKNGQLYPTPTSED 129
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
OY 123 ETVGORALHSILNAAIMISVIVMTLLVLYTKRYCYVIAHMLITSSLLFFPSFTY 182
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 130 PSVQRLNSVNTLIMISVIVMTIFLVLYTKRYCYFIHGMILMSSMLLFFFTY 189
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
OY 183 LGEVFTYVANDYITVALLINLVGMISIMHWKGPLRLOQAYLIMISALMAVFIKYL 242
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 190 GEVLTYYVANDYITVALLINLVGMISIMHWKGPLRLOQAYLIMISALMAVFIKYL 249
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
OY 243 EWTAMLLAVISVYDVLVAVLCRPGRLMVEAQRNRTIFPALYSSMFWLVMAAG 302
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 250 EMSAMVILGALSVDLVAVLCRPGRLMVEAQRNRTIFPALYSSAMVTVMAKL 309
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
OY 303 PEAQRVSKNSKYNAESTERESQDTVAENDDGFSEMEADQSHLGPFRSTPESRAV 362
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 310 PSSQAL--QLPYDPE-MEDSDYSLGE---PSYPEVEAPLPYGP-----E 351
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
OY 363 QELSSSILAGEDEBERGVKLGDFIFYSVLYGKASATASGDMNTTACFVALIGLCT 422
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 352 EL-----EEBERGVKLGDFIFYSVLYGKAAATSGDMNTTACFVALIGLCT 404
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
OY 423 LLLAIFKKALPALPISITFGVFEFATDYLVQPFMDQLAFHQFYI 467
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 405 LLLAIFKKALPALPISITFGVFEFATDYLVQPFMDQLAFHQFYI 449
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 11
PSN2_MOUSE STANDARD: PRT: 448 AA.
ID 061144: P97935; P97934; 054977;
AC 01-NOV-1997 (Rel. 35, Created)
DT 15-01-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Presentin 2 (PS-2) (Alzheimer disease 4 homolog).
GN PSN2 OR PSN2 OR AUC3 OR AD4H OR PS-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
KW MEDLINE=97094860; PubMed=8940094;
RA Vito P., Wolozin B., Ganjel J.K., Iwasaki K., Lacana E., D'Adamo L.;

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[illegible]

OY	3	ELPAPLVSFOQNAQMSMEDHNLSTWTSVQSDNDRQHNDNRSL-GHPPELSNGRPQGNSRQ	61
Db	24	ESPTSRSCQEGPGPDGEDSTRQMWTGQSSEDECDPRAYCSGAP-----GRPSG----	74
OY	62	VVEODEEDELTLTKYGAKKHVIMLEVPATLCVVVVVAATIKSVSFPTRKDGOLIYPFTED	122
Db	75	-----LEEELITLKXGAKRVIMLFEPVTLCIIVVAVAIKSVREFTEKNQGLIYPTFD	122
OY	122	TETVGORALSHILNAAMIMISVIYVMTILLVLYKYRYCKRVIHAWLIISSLLILEFFSFY	18
Db	128	TPSVGOLRLNSVLNTLMISMISVIYVMTIFLVLYLYKYRYCKFIGHGWLIMSMLLEFYIY	18
OY	182	LGEVKRTNVADVTTVALITMNLGVGMGISHHMKGPRLDQAQYIMISALMALVFITYL	24
Db	188	LGEVKRTNVADVDPTLPFLVANNFCGAVCMCIHMGGPALDOAQYIIVSALMALVFITYL	24
OY	242	PEMTAMLIIVASVVDVAVALCPKPRLMLVETAOERNNETLEPALISSYWMLVNMAEG	30
Db	248	PEMSAMVILIIGAISYDLDAVALCPKPLRLMLVETAOERNNEPIPALISSAMVYGMAKL	30
OY	302	DPEAQRVYSKSNKYNAESTERESODTYAENDGGFSEMEARDSHLGPHRSTPESRAAV	36
Db	308	DPSOGAL-QLPYPDP-E MEDSYDSFG- - -PSYPEAFAPALPYPG-----	34
OY	362	QELSSIIAGDEDPBERGYKLGIIDTFYSYLVGKRSATASGDGMTTICFPAAILGLCT	42
Db	350	EEL-----EBEEERGKYLGIIDTFYSYLVGKAATAANGDMTNTLACFIALLIGLCT	40
OY	422	LLLLIPFKALPALPISTFGVPEFANDYLCOPMDLAHFQHYI	467
Db	403	LLLLIPFKALPALPISTFGIIFSTDNLVRPMDTLASHQLYI	448

RESULT 12
PSN2_RAT

ID	PSN2_RAT	STANDARD:	PRT:	448 AA.
AC	088777	035546;	008847;	
DT	15-JUL-1999	(Rel. 38,	Created)	
DT	15-JUL-1999	(Rel. 38,	Last sequence update)	
DT	16-OCT-2001	(Rel. 40,	Last annotation update)	
DE	Presentin 2	(PS-2).		
GN	PSNM2 OR PSNM2	OR PS2.		
OC	Rattus norvegicus (rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus			
OX	NCBI_Taxid=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-Wistar; TISSUE-Brain;			
RA	Fretzel S., Abdel A.S., Luebert H.;			
RL	Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-Wistar; TISSUE-Brain;			
RX	MEDLINE-97473536; PubMed=9332390;			
RA	Takahashi H., Mecken M., Nakazato Y., Noguchi K., Murayama M.,			
RA	Imaiori K., Takashima A.;			
RT	"Cloning of cDNA and expression of the gene encoding rat			
RT	presentin-2.";			
RL	Gene 197:383-387(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-Wistar; TISSUE-Brain;			
RX	MEDLINE-98207716; PubMed=9545577;			
RA	Tanahashi H., Tabira T.;			
RT	"Cloning of the cDNA encoding rat presentin-2.";			
RL	Biochim. Biophys. Acta 136:259-262(1998).			
CC	-I- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE			
CC	EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE. MAY			
CC	FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS (BY			
CC	SIMILARITY).			
CC	-I- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A			
CC	C-TERMINAL (CTF) ENDOPROTEOLYTICAL FRAGMENT (BY SIMILARITY).			

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, GOLGI AND
CC ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PRESENTLIN FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X99267; CAA67663.1; -
DR EMBL: D83700; BAA22832.1; -
DR EMBL: AB004454; BAA20406.1; -
DR MEROPS: A22.002; -
DR InterPro: IPR001108; Presentlin.
DR Pfam: PF01080; Presentlin; 1.
DR PRINTS: PR01072; PRESENTLIN.
KW Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack.
FT CHAIN 1 297 PRESENTLIN 2 NTF SUBUNIT (BY SIMILARITY).
FT DOMAIN 298 448 PRESENTLIN 2 CTF SUBUNIT (BY SIMILARITY).
FT TRANSMEM 1 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 106 POTENTIAL.
FT TRANSMEM 107 141 LUMENAL (POTENTIAL).
FT TRANSMEM 142 159 LUMENAL (POTENTIAL).
FT TRANSMEM 160 166 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 188 POTENTIAL.
FT DOMAIN 189 202 LUMENAL (POTENTIAL).
FT TRANSMEM 203 219 POTENTIAL.
FT DOMAIN 220 229 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 230 246 POTENTIAL.
FT TRANSMEM 247 252 LUMENAL (POTENTIAL).
FT TRANSMEM 253 269 POTENTIAL.
FT DOMAIN 270 386 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 387 406 POTENTIAL.
FT TRANSMEM 414 434 S -> T (IN REF. 1).
FT CONFLICT 7 87 KH -> ND (IN REF. 3).
FT CONFLICT 86 87
SQ SEQUENCE 448 AA; 50051 MW; 299A7C416405046C CRC64;

Query Match 60.2%; Score 1439; DB 1; Length 448;
Best Local Similarity 63.9%; Pred. No. 4,8e-88;
Matches 298; Conservative 44; Mismatches 82; Indels 42; Gaps 7;

OY 3 ELPAPISTYONAMQSEDNHLSNTRSONDRREHNDKRSI-GHEPPLNKGPOQNSQ 61
DB 24 EESTSRSCDSRPEDGENTAGMRQSENDDEDDPDHYACSGVP-----GRPSG---- 74
OY 62 VVEQDEEDELTLKYGAKHVMLEFVPTLCMVVVVATIKSVSEYTRKDGOLITPTPTD 121
DB 75 -----LEBELTKYGAHVMLEFVPTLCMVVVVATIKSVSEYTRKDGOLITPTPTD 127
OY 122 TETVGORALHSIIAAIMISVIVMTILLVLYKYRCYVIAHMLIISLLLFPSFTY 181
DB 128 TTSVGORLINSVLTIMISVIVMTILFVLYKYRCYFIHGLIMLSMLLFPTIY 187
OY 182 LGVEFTYVAVDYITVALLIMLGVGMISTHMKRPLAQAYLIMISALMAVYIKTL 241
DB 188 LGVEFTYVAVDYITVALLIMLGVGMISTHMKRPLAQAYLIMISALMAVYIKTL 247
OY 242 PENTANLILAVISYVDVAVLCRGPRLMIVETAQRNETLFPALISSYTMVLYMAG 301
DB 248 PEKSAVILIGALISYVDVAVLCRGPRLMIVETAQRNETLFPALISSYTMVLYMAG 307
OY 302 DPAQRVSKNSKYNAESTERESQDTVAENDGSESEMEPAQDSHLGHRSTPESRAV 361
DB 308 DSSSQAL--QLPYDPE-MEEDSYDSFGE---PSYPEAPEAPQPGYGBE----- 351
OY 362 QELSSSIIAGDEPERGVVLGLGDFIFYSVLGKASATSGMNTIACFAVAILIGLCT 421
DB 352 -----PEEEERGVLGLGDFIFYSVLGKAAATGNGMSTIACFAIILIGLCLT 402

OY 422 LLLALFKKALPALPISITFGLVEFATDYVOPFMDOLAFHOFYI 467
DB 403 LLLAVFKKALPALPISITFGLIFYSTDLNVRPFMDLASHQLYI 448

RESULT 13
PSN_DROME STANDARD; PRT; 541 AA.
ID PSN_DROME 002395; 076802; 09V319; 09TY80; 09V3S1; 096340;
AC 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Presentlin homolog (DPS) (DMPs).
GN PSN OR PS OR CG18803/CG5868.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND DEVELOPMENTAL STAGE.
RC TISSUE-Embryo.
RX MEDLINE-9728368; PubMed-9141085;
RA Boulianne G.L., Liyne-Bar I., Humphreys J.M., Liang Y., Lin C.,
Rogaev E., St George-Hyslop P.H.;
RT "Cloning and characterization of the Drosophila presentlin
RT homolog.";
RL NeuroReport 8:1025-1029(1997).
RN [2]
RP SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE (SHORT ISOFORM).
RC STRAIN-Canton-S; TISSUE-Embryo, and Head;
RX MEDLINE-97260623; PubMed-9106743;
RA Hong C.-S., Koo E.H.;
RT "Isolation and characterization of Drosophila presentlin homolog.";
RL NeuroReport 8:665-668(1997).
RN [3]
RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS), TISSUE SPECIFICITY,
RP DEVELOPMENTAL STAGE, SUBCELLULAR LOCATION, AND ALTERNATIVE SPLICING.
RX MEDLINE-99279250; PubMed-10349633;
RA "Characterization of Drosophila Presentlin and its colocalization with
RA ye Y., Fortini M.E.;
RT Notch during development.";
RL Mech. Dev. 79:199-211(1998).
RN [4]
RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
RX MEDLINE-99221488; PubMed-10206647;
RA ye Y., Lukinova N., Fortini M.E.;
RT "Neurogenic phenotypes and altered Notch processing in Drosophila
RT presentlin mutants.";
RL Nature 398:525-529(1999).
RN [5]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND DEVELOPMENTAL STAGE.
RC STRAIN-Canton-S;
RX MEDLINE-98331525; PubMed-9666900;
RA Marfany G., Del-Pavero J., Valero R., De Jonghe C., Woodrow S.,
Hendriks L., Van Broeckhoven C., Gonzalez-Duarte R.;
RT "Identification of a Drosophila presentlin homologue: evidence of
RT alternatively spliced forms.";
RL J. Neurogenet. 12:41-54(1998).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE-99423881; PubMed-10493744;
RA Guo Y., Liyne-Bar I., Zhou L., Boulianne G.L.;
RT "Drosophila presentlin is required for neuronal differentiation and
RT affects notch subcellular localization and signalling.";
RL J. Neurosci. 19:8435-8442(1999).
RN [7]
RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
RC STRAIN-Berkeley;
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Ceindler S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Bateman A., Rogers Y.-H.C., Blazet J.R.G., Chape M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dudin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shie B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE PATTERNING OF THE
CC OPTIC LOBES. PROTEIN MAY ACT, TOGETHER WITH NOTCH, TO SPECIFY
CC CELL FATES THROUGHOUT DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC ENOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM/PS-D; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: MATERNALLY EXPRESSED IN NURSE AND FOLLICLE
CC CELLS. IN EARLY EMBRYOS, EXPRESSED IN ALL OR MOST CELLS AND LATER
CC INCREASES IN CNS AND EPIDERMAL TISSUES. IN LARVAE, EXPRESSION IS
CC SEEN IN ALL IMAGINAL DISKS, BRAIN AND OPTIC LOBES. IN PUPAE,
CC EXPRESSION IS SEEN IN EYE DISK AND BRAIN.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY
CC THROUGHOUT DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE PRESENTLIN FAMILY.
CC -----
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CC -----
CC EMBL: U77934; AAB6139.1; -;
CC EMBL: U78084; AAB53369.1; -;
CC EMBL: AF084184; AAC33129.1; -;
CC EMBL: AF084184; AAC33128.1; -;
CC EMBL: AF017024; AAD01610.1; -;
CC EMBL: AF017025; AAD01611.1; -;
CC EMBL: AF017026; AAD01612.1; -;
CC EMBL: AF093402; AAD52707.1; -;
CC EMBL: AF093402; AAD52708.1; -;
CC EMBL: AE003591; -; NOT ANNOTATED_CDS.
CC EMBL: AE003591; AAF51596.1; -;
CC DR MEROPS: A2.0WF; -;
CC FlyBase: FBgn0019947; Psn.

DR InterPro: IPR001108; Presentlin.
DR Pfam: PF01080; Presentlin.1.
DR PRINTS: PR01072; Presentlin.
KW Transmembrane; Glycoprotein; Alternative splicing.
FT TRANSMEM 107 127 POTENTIAL.
FT TRANSMEM 155 175 POTENTIAL.
FT TRANSMEM 183 203 POTENTIAL.
FT TRANSMEM 217 237 POTENTIAL.
FT TRANSMEM 243 263 POTENTIAL.
FT TRANSMEM 266 286 POTENTIAL.
FT TRANSMEM 304 324 POTENTIAL.
FT TRANSMEM 482 502 POTENTIAL.
FT TRANSMEM 507 527 POTENTIAL.
FT CARBOHD 129 129 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHD 339 339 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHD 410 410 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPLIC 384 397 MISSING (IN SHORT ISOFORM).
FT CONFLICT 80 81 GG -> RS (IN REF. 2).
SQ SEQUENCE 541 AA; 59304 MW; A3B3D54348A2C03F CRC64;
Query Match 49.2%; Score 1177.5; DB 1; Length 541;
Best Local Similarity 47.5%; Pred. No. 11e-70;
Matches 251; Conservative 73; Mismatches 125; Indels 79; Gaps 9;
QY 17 SED-----NHLNTRYQNDNREDEHNDRLSGHPEPLS-----NGRPQ- 56
DB 16 SEDDANVSGQIAERLEPPRROQRNNYSGSNDQPPAAILAVPNVVMRECGSR 75
QY 57 ---GNSROYEDDEDEDELLTKGAKHVMLEPVTLQVNVVATIKSVFTRRGG 113
DB 76 LINGGGGSGCPPTNEEEQGLKYGQHVIKLFVPSLCMLVAVATINSIFNSDVL 135
QY 114 ITPPTDEETYGQRLSHILNAIMISIVYITLLVLYXKRCYKHAMLIISLL 173
DB 136 LTPPEQSPSPSVKFWSLANSLIMSVVWTFLLVLYKRCYRIIHGWLISSEFL 195
QY 174 LFFFSFIYGEVFKTYNAVVDYITVALLIMNGVGMISHHKGPRLQOAVLIMISALM 233
DB 196 LFIPIYLYEELLRATVINIMDPTALLIMNGVGMISHHKGPRLQOAVLIMISALM 255
QY 234 ALVFIKYLEPTWALVLIAVISYDLVAVLCPKGPLMALVETAOERNETLPAALISSTV 293
DB 256 ALVFIKYLEPTWALVLIAVISYDLVAVLCPKGPLMALVETAOERNETLPAALISSTV 315
QY 294 W-LVMAEEDPEAQRVNSKYNKNESTERESODPTA-----END 332
DB 316 VALVNTVTPQSOATRASSPSSNSTTTRATONSILASPEAALASGQRTGNSHPROMRD 375
QY 333 DC-----GFSEWEDAQRDSHLQPH---RSTPESRAVQEL 364
DB 376 DCSVLATGEMPLVTPKSNLRGNAEAAGFTQBSANLSEVAVARQIEVOSTGSMORSM 435
QY 365 SSSIIAGED-----PEERGVLGLGDFIFYSVLVGKASATASGDMNTTACFVAILIGLC 419
DB 436 YRTVYAPDQNHDPDQGEERIKLGLDFIFYSVLVGKAS--SYGDMNTTACFVAILIGLC 493
QY 420 LLLLLATKRALPALPISITGIVYFATDVLVQFPMOQLAFHOYI 467
DB 494 LLLLLATKRALPALPISITGILFCFATSVAVKPEMELSAKOVFI 541
RESULT 14
ID PSN_CAEEL STANDARD; PRT; 444 AA.
AC P52166; Q20076; Q909C7;
DT 01-OCT-1996 (Rel. 34; Created)
DR 15-JUN-2002 (Rel. 41; Last sequence update)
DT 15-JUN-2002 (Rel. 41; Last annotation update)
DE Presentlin sel-12.
GN SEL-12 OR F35H12.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderae; Caenorhabditis.

OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT SER-60.
 RC STRAIN-Bristol N2;
 RX MEDLINE=96032531; PubMed=7566091;
 RA Levitan D., Greenwald I.,
 RT "Facilitation of lin-12-mediated signalling by sel-12, a
 Caenorhabditis elegans S182 Alzheimer's disease gene.";
 RL Nature 377:351-354(1995).
 RN [2]
 RP REVISIONS TO 84-85.
 RA Levitan D.,
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
 RC STRAIN-Bristol N2;
 RX MEDLINE=20372200; PubMed=10917532;
 RA Wittenburg N., Elmer S., Lakowski B., Roehrig S., Rudolph C.,
 RA Baumeister R.,
 RT "Presenilin is required for proper morphology and function of neurons
 in C. elegans.";
 RL Nature 406:306-309(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RL Nelson J., Gattung S.,
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP REVISIONS.
 RA Waterston R.,
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAY FACILITATE LIN-12 MEDIATED RECEPTION OF
 INTERCELLULAR SIGNALS. IT MIGHT BE DIRECTLY INVOLVED IN LIN-12
 DOWNSTREAM EFFECTOR THAT IS ACTIVATED UPON LIN-12 ACTIVATION.
 CC ALTERNATIVELY IT MAY BE INVOLVED IN A MORE GENERAL CELLULAR
 PROCESS SUCH AS RECEPTOR LOCALIZATION OR RECYCLING. AND HENCE
 INFLUENCE LIN-12 ACTIVITY INDIRECTLY. Required cell-autonomously
 for correct neurite connectivity of the A1y cholinergic
 interneurons and their correct functioning in thermotaxis.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in most neurons.
 CC -1- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: U35660; AA05511.1; -;
 DR EMBL: AF171064; AND05091.1; -;
 DR EMBL: U01340; AAK39230.1; -;
 DR MEROPS: A22.0PW; -;
 DR WormBep: F35H12.3; CE24946.
 DR InterPro: IPR001686; Nema-presenilin.
 DR InterPro: IPR001108; Presenilin.
 DR Pfam: PF01080; Presenilin_1.
 DR PRINTS: PRO1072; PRESENILIN.
 DR PRINTS: PRO1075; PRESENILINSEL.
 KW Transmembrane.
 FT TRANSMEM 46 66 POTENTIAL.
 FT TRANSMEM 102 122 POTENTIAL.
 FT TRANSMEM 131 151 POTENTIAL.
 FT TRANSMEM 164 184 POTENTIAL.
 FT TRANSMEM 190 210 POTENTIAL.
 FT TRANSMEM 213 233 POTENTIAL.
 FT TRANSMEM 251 271 POTENTIAL.
 FT TRANSMEM 385 405 POTENTIAL.
 FT TRANSMEM 60 60 POTENTIAL.
 FT VARIANT 413 444 C -> S (IN AR131; EGG-LAYING-DEFECTIVE).
 FT CONFLICT 413 444 PISFSGLIFFCTRWITTPYVVSOKCLLY -> QPFPFS

FT PSEFTVPAGSSPHLLHKSLSVYINSLEFLPCLINFS
 FT ITS (IN REF. 1).
 SQ SEQUENCE 444 AA; 50034 MW; 37ADB0C124E16429C CRC64;
 Query Match 44.38; Score 1059.5; DB 1; Length 444;
 Best Local Similarity 51.48; Pred. No. 5,2e-63;
 Matches 218; Conservative 71; Mismatches 92; Indels 43; Gaps 7;
 OY 64 EODEEDELTLGKAGKATMLFVPTLCWVAVATKSYSPYTRKQD-LIYTPFEDT 122
 DB 32 QEDENVEEALTKGASHVHLFVPSLCMALVFTNTTFFSQNGRHLITTPFRET 91
 OY 123 ETVGORALSHILNAAMISVIVMTLLVLYKRCXYIHAMLISSLLLEFFSEIYL 182
 DB 92 DSIVKGLMSLGNALVLMCVLMTVLLIYVEYKFKYKFLHGMILYSSFLLEFFETIY 151
 OY 183 GEVFKITNAVVDYITVALIMNIGVGMISIHMKGPLRLOQATLIMSALMALVFIKYL 242
 DB 152 QEVLSFSDVSPSALVLFEGNGYGLGMCIMHKGPLRLOQFYLIMSALMALVFIKYL 211
 OY 243 EMTAMLIIVSYVDVAVCPKGPLRMLVETAOERRETLFPALITYSSTMW---LVNMA 299
 DB 212 EMTVWFVLFVYSWDLVAVLTPKGPLRYLVETAOERNEPFLPALITYSGVIYVLYTAV 271
 OY 300 EGDPEAQRYVSKNS-----KYNAESTER-----ESDPTVAENDGGS 337
 DB 272 ENTTPDREPTSDSNSTAFPGEASCSSEPKPKYKRIQKVQISNTFTASTQNSGVR 331
 OY 338 EEMEAQRDHLGHRSPESRAAVQELSSILAGEPDEEGVNLGDFLFYSVLGKAS 397
 DB 332 VE-----RELAAERPTVODAN---FHRHEEERGVKLGDFLFYSVLGKAS 376
 OY 398 ATSGDMNTTIFACEVAILLICLTLLLAIFKRALPALPSTIFFGVYFATGYLOVOPM 457
 DB 377 SYF--DMNTTIACVAILLICLTLLVLAIFKRALPALPSTISGLIFTCMTIITP 434
 OY 458 DQEA 461
 DB 435 TVGS 438
 RESULT 15
 PSNH_ARATH STANDARD; PRT; 453 AA.
 AC 064668;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Presenilin homolog.
 GN A11G08700 OR F22013.18.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-cv. Columbia;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chen Q., Chen R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Egu P., Feldblum T.V., Feng J.-D., Feng B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marzilli A.,
 RA Miltischer J., Miranda M., Nguyen M., Nguyen W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Taiton L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
FT thaliana";
RL Nature 408:816-820(2000).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
CC -----
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CC -----
DR EMBL; AC003981; AAF9776.1; -.
DR MEROPS; A2.0PW; -.
DR InterPro; IPR001108; Presenilin.
DR Pfam; PF01080; Presenilin; 1.
DR PRINTS; PR01072; PRESENILIN.
KM Transmembrane.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 69 89 POTENTIAL.
FT TRANSMEM 104 124 POTENTIAL.
FT TRANSMEM 133 153 POTENTIAL.
FT TRANSMEM 160 180 POTENTIAL.
FT TRANSMEM 181 201 POTENTIAL.
FT TRANSMEM 370 390 POTENTIAL.
FT TRANSMEM 393 413 POTENTIAL.
FT TRANSMEM 418 438 POTENTIAL.
SQ SEQUENCE 453 AA; 49308 MW; 7EBDD9886D97955E CRC64;

Query Match 22.98; Score 546.5; DB 1; Length 453;
Best Local Similarity 33.38; Pred. No. 3,7e-29;
Matches 146; Conservative 76; Mismatches 146; Indels 71; Gaps 14;

QY 82 VIMLEVPVTCMNVVYVATIKSVSYT---RKDGQLYTPTEDDETETGGRALHSILNAA 137
DB 13 IIGVMAFVSICMFLVLLTYSLSVTSPOIRSAANLIYIENPSDSTTV--KLEGSLANAI 70
QY 138 IMISVIVVMTLLVLLVLYKRYKVIHAWLISSLLLEFFSFYLGVEFKYNAVVDYIT 197
DB 71 VEVVLIAAVPIFLVLLFYNTNFKHYMRSAFVLTGMCALFSLIQHFSIPVDSIT 130
QY 198 VALLIMNLGVVGMISIMKKG-PLRLQAYLIMISALNALVFIKYLPEWTAWLITAVISVY 256
DB 131 CFILLFNFITLIGTLSEFAGGIPIVLRQCYVVMGIVVAAMFTK-LPEWTWFIIVLALY 189
QY 257 DLVAVILCPKGLRLVLETAQDRNETLFPALY-----SSTWVMLVN--- 297
DB 190 DLVAVILAPGGPLKLLVELASSRDEL--PAMVYEAPVYSSGNORNRGSSLRALVGGGV 248
QY 298 MAEGDPPEAQ-----RRVSKNSKYNASTE--RESQDTVAENDDGGFSEE----- 339
DB 249 SDGSSVELQANRNHDVQNLGRENHNDYNAIAVRDIDNVDDIGNGSRGLERSPLVGS 308
QY 340 -WEAQRDSHLGPARSTPESRAAVQELSSILA-----GEDEPE-----RG 378
DB 309 PSASEHSTSVGT-RGNMEDRESVMEDEMSPLVELMGWGDNRREARGLESDNVVDISNRG 367
QY 379 VKIGLGPFIFFSVYVKASATASGDWNTTACFAVAILGLCTLLLLAIFKALPALPIS 438
DB 368 IKIGLGPFIFFSVYLVGRA--AMYDLMTYVACYLAIISGLCTLLLSVYNRALPALPIS 424
QY 439 ITFGLVFFATDYLVQPEM 457
DB 425 IMIGVVFYFLRLLMPEFV 443

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GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 19:20:04 ; Search time 58 Seconds
(Without alignments)
1659.035 Million cell updates/sec

Title: US-09-689-159a-2
Perfect score: 2391
Sequence: 1 MTELPAPLSYFQNAQMSQDN.....ATDYLQPFMDQLAFHQFYI 467

Scoring table:
BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1984.5	83.0	468	13	090X08 090X08 gallus gall
2	1616	67.6	378	4	096P33 096P33 homo sapien
3	1612.5	67.4	456	13	09W6T7 09W6T7 brachydanio
4	1527.5	63.9	384	13	073869 073869 cyprinus ca
5	1473	61.6	289	4	09UIR0 09UIR0 homo sapien
6	1445	60.4	448	11	091VS3 091VS3 mus musculu
7	1418	59.3	441	13	090Z64 090Z64 brachydanio
8	1417	59.3	441	13	09191 09191 brachydanio
9	1370	57.3	504	5	08WS58 08WS58 branchiosto
10	1368.5	57.2	451	13	090X07 090X07 gallus gall
11	1362.5	52.0	582	5	08WS59 08WS59 branchiosto
12	1243.5	52.0	582	5	09GUS8 09GUS8 helix lucor
13	1221	51.1	261	11	091WK6 091WK6 mus musculu
14	1188	49.7	390	4	096P32 096P32 homo sapien
15	952.5	39.8	332	11	09D616 09D616 mus musculu
16	828.5	34.7	184	4	095465 095465 homo sapien

17	568	23.8	478	10	09SD62 09SD62 oryza sativ
18	539	22.5	397	10	09S1K7 09S1K7 arabidopsis
19	153	6.4	291	17	08X12 08X12 pyrobaculum
20	127.5	5.3	338	5	09G514 09G514 caenorhabdi
21	125.5	5.2	691	4	09HAS3 09HAS3 homo sapien
22	123.5	5.2	455	16	097FJ2 097FJ2 clostridium
23	120.5	5.0	309	16	098QF5 098QF5 mycoplasma
24	118.5	5.0	305	4	096A60 096A60 homo sapien
25	117	4.9	224	2	08V5X2 08V5X2 staphylococ
26	115.5	4.8	339	17	058554 058554 pyrococcus
27	114	4.8	318	17	09H023 09H023 halobacteri
28	114	4.8	417	16	08RH68 08RH68 fusobacteri
29	112	4.7	410	2	0939W3 0939W3 aeromonas s
30	111	4.6	705	11	08V1R3 08V1R3 rattus norv
31	110.5	4.6	598	10	082747 082747 arabidopsis
32	110	4.6	601	5	095YF4 095YF4 drosophila
33	109	4.6	389	16	092810 092810 listeria in
34	108	4.5	291	16	0981C7 0981C7 rhizobium l
35	108	4.5	364	16	092U24 092U24 rhizobium m
36	108	4.5	419	4	08TDV0 08TDV0 homo sapien
37	108	4.5	578	2	09RMD0 09RMD0 calobacter
38	107.5	4.5	269	2	09WVX0 09WVX0 pediococcus
39	107	4.5	835	4	09ULF5 09ULF5 homo sapien
40	106.5	4.5	317	17	097CM0 097CM0 thermoplas
41	105.5	4.4	699	10	093Z05 093Z05 arabidopsis
42	105	4.4	616	8	09G859 09G859 malawimonas
43	104.5	4.4	224	2	08V5X5 08V5X5 staphylococ
44	104	4.3	583	5	09VNZ5 09VNZ5 drosophila
45	104	4.3	599	5	022089 022089 caenorhabdi

ALIGNMENTS

RESULT 1	ID	Q90X08	PRELIMINARY:	PRT:	468 AA.
AC	Q90X08:				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)				
DE	Presentinlin 1.				
OS	Gallus gallus (Chicken).				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
CC	Gallus.				
OX	NCBI_taxid=9031;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=EL4; TISSUE=BRAIN;				
RA	Korade Mirnics Z., Kerjanov S., Lovelock J., Corey S.J.;				
RT	"Cloning of chicken presentinlin."				
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AY043492; AAK95408.1; -				
DR	InterPro: IPR001108; Presentinlin.				
DR	Pfam: PF01080; Presentinlin; 1.				
DR	PRINTS: PR01072; PRESENTLIN.				
SO	SEQUENCE 468 AA; 52812 MW; B746BEDA3BAC0BFA CRC64;				
Query Match	83.0%; Score 1984.5; DB 13; Length 468;				
Best Local Similarity	83.3%; Pred. No. 2.9e-157;				
Matches	393; Conservative 29; Mismatches 41; Indels 9; Gaps 3;				
Oy	1 MTELPAPLSYFQNAQMSF---DNHLSNTVRSQNDNRROEH--NDRSLGHPPLSNGRP 55				
Db	1 MTELSAHLPOFGHGTENFPDNLSTNT---NDNSERRRHSERRRNDNGSTNOOP 56				
Oy	56 OGNRSQVVEODEEEDDELTGKAGKAVIMLFPVTLCAVVVAVATKSVSFYRKQGLIY 115				
Db	57 ONNIOQVVDDEDEDELTGKAGKAVIMLFPVTLCAVVVAVATKSVSFYRKQGLIY 116				
Oy	116 TPTFEDTFVGQRALSHLNAIMISVIVMTLLVLYKYCYVVIHAMLISLLLF 175				

DB 117 TPTETETITGGRALNSIINAAIMISVITVLLVLYKYRCYKVIHGMILISLLILF 176
QY 176 FFSFIYLGVEFKTYNVAVDYITVALLIMNLGVGMISIMHKGPRLQOAYLIMISALMAL 235
DB 177 FFSFIYLGVEFKTYNVAVDYITVALLIMNLGVGMISIMHKGPRLQOAYLIMISALMAL 236
QY 236 VFETKYLPENTAMILLAVISYVDLVAVLCPRKPLMLVETAOERNEETLFPALIVSSITWML 295
DB 237 VFETKYLPENTAMILLAVISYVDLVAVLCPRKPLMLVETAOERNEETLFPALIVSSITWML 296
QY 296 VNNAEGDPEAORRVSNSKYNAESTERESODTYAENDDGFSEMEQROSDSHGPHRSTP 355
DB 297 VNNAEGDPEAORRVSNSKYNAESTERESODTYAENDDGFSEMEQROSDSHGPHRSTP 356
QY 356 ESRAAVQELSSITLAGEDEBERGVKLGIDFIETYSVLVKASATASGDMNTTITACFVAL 415
DB 357 ESRAAVQELSSITLAGEDEBERGVKLGIDFIETYSVLVKASATASGDMNTTITACFVAL 416
QY 416 IGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVOPEMDQLAFHOPI 467
DB 417 IGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVOPEMDQLAFHOPI 468

RESULT 2

ID Q96P33 PRELIMINARY; PRT; 378 AA.
AC Q96P33; 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DR 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Presentinlin 1.
GN PSEN1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kang L., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.;
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF416717; AAL16811.1; -
DR InterPro; IPR001108; Presentinlin.
DR Pfam; PF01080; Presentinlin; 1.
DR PRINTS; PRO1072; PRESENTLIN.
SQ SEQUENCE 378 AA; 42658 MW; A09D6D2FC6F5618D CRC64;

Query Match 67.6%; Score 1616; DB 4; Length 378;
Best Local Similarity 99.4%; Pred. No. 1,2e-126;
Matches 316; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPELPAPLSYFQNAQNSQEDNHLSTNVRSONDNREQEHNDRLSLGHPEPLSNGRPOGNSR 60
DB 1 MPELPAPLSYFQNAQNSQEDNHLSTNVRSONDNREQEHNDRLSLGHPEPLSNGRPOGNSR 60
QY 61 QVVEQDEEDELTLTKYGAHVIMLFVPTLCMVVVAVATIKSVSFTRDGOQLITPFTF 120
DB 61 QVVEQDEEDELTLTKYGAHVIMLFVPTLCMVVVAVATIKSVSFTRDGOQLITPFTF 120
QY 121 DIETVQGRALHSLINAIMISVIVMTLLVLYKYRCYKVIHGMILISLLILFESSFI 180
DB 121 DIETVQGRALHSLINAIMISVIVMTLLVLYKYRCYKVIHGMILISLLILFESSFI 180
QY 181 YLGEVEFKTYNVAVDYITVALLIMNLGVGMISIMHKGPRLQOAYLIMISALMALVFIKY 240
DB 181 YLGEVEFKTYNVAVDYITVALLIMNLGVGMISIMHKGPRLQOAYLIMISALMALVFIKY 240
QY 241 LPEWTAMILLAVISYVDLVAVLCPRKPLMLVETAOERNEETLFPALIVSSITWMLVNAE 300
DB 241 LPEWTAMILLAVISYVDLVAVLCPRKPLMLVETAOERNEETLFPALIVSSITWMLVNAE 300
QY 301 GDEAORRVSNSKYNAE 318
DB 301 GDEAORRVSNSKYNAE 318

RESULT 3
ID Q9W6T7 PRELIMINARY; PRT; 456 AA.
AC Q9W6T7; 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DR 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Presentinlin-1.
GN PSEN.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Leimer U., Haass C.;
RT "Expression, proteolytic processing, and amyloidogenic activity of
zebrafish (Danio rerio) presentinlin-1.";
RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ132931; CAB40386.1; -
DR MEROPS; A22.001; -
DR ZFIN; ZDB-GENE-991119-4; psen.
DR InterPro; IPR001108; Presentinlin.
DR Pfam; PF01080; Presentinlin; 1.
DR PRINTS; PRO1072; PRESENTLIN.
SQ SEQUENCE 456 AA; 50981 MW; B90C42280C874F8D CRC64;

Query Match 67.4%; Score 1612.5; DB 13; Length 456;
Best Local Similarity 71.9%; Pred. No. 3e-126;
Matches 333; Conservative 33; Mismatches 78; Indels 19; Gaps 7;

QY 12 QNAQNSQEDNHLSTNVRSONDNREQEHNDRLSLGHPEPLSNGRPOGNSQVY-EDDEED 70
DB 6 QNAQNSQEDNHLSTNVRSONDNREQEHNDRLSLGHPEPLSNGRPOGNSQVY-EDDEED 58
QY 71 EELTLTKYGAHVIMLFVPTLCMVVVAVATIKSVSFTRDGOQLITPFTETETVGGRA 129
DB 59 EELTLTKYGAHVIMLFVPTLCMVVVAVATIKSVSFTRDGOQLITPFTETETVGGRA 118
QY 130 LHSILNAIMISVIVMTLLVLYKYRCYKVIHGMILISLLILFESSFIYLGVEFKTY 189
DB 119 LHSILNAIMISVIVMTLLVLYKYRCYKVIHGMILISLLILFESSFIYLGVEFKTY 178
QY 190 NVAVDYITVALLIMNLGVGMISIMHKGPRLQOAYLIMISALMALVFIKYLPENTAMLI 249
DB 179 NVAVDYITVALLIMNLGVGMISIMHKGPRLQOAYLIMISALMALVFIKYLPENTAMLI 238
QY 250 LAVISYVDLVAVLCPRKPLMLVETAOERNEETLFPALIVSSITWMLVNNAEGDPEAORRV 309
DB 239 LAVISYVDLVAVLCPRKPLMLVETAOERNEETLFPALIVSSITWMLVNNAEGDPEAORRV 294
QY 310 SKNSKYNAESTERE--SODTYAENDDGFSEMEQROSDSHGPHRSTPESRAAVQELSS 366
DB 295 SKNSKYNAESTERE--SODTYAENDDGFSEMEQROSDSHGPHRSTPESRAAVQELSS 353
QY 367 S--TLAGEDEBERGVKLGIDFIETYSVLVKASATASGDMNTTITACFVALILGLCLTLL 424
DB 354 ARPPPADDEBERGVKLGIDFIETYSVLVKASATASGDMNTTITACFVALILGLCLTLL 413
QY 425 LAIFKKALPALPISITFGLVFYFATDYLVOPEMDQLAFHOPI 467
DB 414 LAIFKKALPALPISITFGLVFYFATDYLVOPEMDQLAFHOPI 456

RESULT 4
ID Q73869 PRELIMINARY; PRT; 384 AA.
AC Q73869; 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE PSI protein (Fragment).
 GN PSI.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 OX NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-9637349; PubMed-9674592;
 RA Archer S., Hirano J., Diss J.K.J., Fraser S.P., Djamgoz M.B.A.;
 RT "Expression and localization in the fish retina of a homologue of the
 RL Alzheimer's related PSI gene";
 RL Neuroreport 9:2049-2056(1998).
 DR EMBL: Y17128; CAA76641.1; -;
 DR MEROPS: A22.001; -;
 DR InterPro: IPR001108; Presentinlin.
 DR Pfam: PF01080; Presentinlin; 1.
 DR PRINTS: PR01072; PRESENTLIN.
 FT NON_TER 1 1
 FT VARIANT 5 5 I -> V.
 FT VARIANT 56 56 A -> S.
 FT VARIANT 56 56 A -> V.
 FT VARIANT 60 60 S -> G.
 FT VARIANT 63 63 V -> L.
 FT VARIANT 83 83 G -> A.
 FT VARIANT 118 118 A -> S.
 FT VARIANT 200 200 P -> T.
 SQ SEQUENCE 384 AA; 43276 MM; F97EEFE24B31FDA CRC64;

Query Match 63.9%; Score 1527.5; DB 13; Length 384;
 Best Local Similarity 79.3%; Pred. No. 3e-119;
 Matches 310; Conservative 28; Mismatches 40; Indels 13; Gaps 6;

OY 83 IMLEPVTLCAVVVAVATIKSVSEYTRKDG-OLITPTEDTETVGORALSHSLNAIMIS 141
 DB 1 IMLEFPTVLCMVVAVATIKSVSEYTRKDGOLITPTEDTETVGORALSHSLNAIMIS 60
 OY 142 VIVVNTLLVLYKRCYKVIHAWLISSLLFFSFYIGEVKRYTNVANDYITVAL 201
 DB 61 VIVVNTLLVLYKRCYKVIHAWLISSLLFFSFYIGEVKRYTNVANDYITVAL 120
 OY 202 IWNLCVGMISIHMKGPLRLOQAYLIMISALMALVFIKLPENTAMLIAYSYDLAV 261
 DB 121 IWNLCVGMISIHMKGPLRLOQAYLIMISALMALVFIKLPENTAMLIAYSYDLAV 180
 OY 262 LCPKGPLMLVETAGERNETLEPALIYSTVMVLMVMAEGDEAQRVSKNSKNAESTE 321
 DB 181 LCPKGPLMLVETAGERNETLEPALIYSTVMVLMVMAEGDEAQRVSKNSKNAESTE 233
 OY 322 RESOOTVA---ENDDGFSEMEAMORSHLGPHESTPESRAAVDELSSILAG-EDPEE 376
 DB 234 QENDAVAPYQOPEDDGTTPAWVNOQHQLGPMOSTEDSRREIDLPBARPPVEDDEE 293
 OY 377 RGVKLGIDLFYSLVKASATASGDNNTTACFAVILIGLCTLLLLAIFKALPALP 436
 DB 294 RGVKLGIDLFYSLVKASATASGDNNTTACFAVILIGLCTLLLLAIFKALPALP 353
 OY 437 ISTFGVLFYATDYLVOPFMDQAFHOFYI 467
 DB 354 ISTFGVLFYATDYLVOPFMDQAFHOFYI 384

RESULT 5
 O9UIF0 PRELIMINARY; PRT; 289 AA.
 AC O9UIF0;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-DEC-2001 (Tremblrel. 13, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE Presentinlin 1 (Fragment).
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99063792; PubMed-9847074;
 RA Sulston J.E., Waterston R.;
 RT "Toward a complete human genome sequence.";
 RL Genome Res. 8:1097-1108(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kozlowicz A., Pape R., Biewald T.;
 RT "The sequence of Homo sapiens PAC clone RP4-687K1.";
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RA Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AC004858; AAF19253.1; -;
 DR InterPro: IPR001108; Presentinlin.
 DR Pfam: PF01080; Presentinlin; 1.
 DR PRINTS: PR01072; PRESENTLIN.
 FT NON_TER 289 289
 SQ SEQUENCE 289 AA; 33067 MM; D503395A31C0EBCB CRC64;

Query Match 61.6%; Score 1473; DB 4; Length 289;
 Best Local Similarity 99.7%; Pred. No. 7.4e-115;
 Matches 288; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MTELPAPLSYFONAOSEDNHLSNTVRSQNDNREROENHNDRLSGHPEPLSNGRPGNSR 60
 DB 1 MTELPAPLSYFONAOSEDNHLSNTVRSQNDNREROENHNDRLSGHPEPLSNGRPGNSR 60
 OY 61 QVVEDDEDEDELTLYKAKHYIMLPVYTLQVVVAVATIKSVSEYTRKDGOLITPTPE 120
 DB 61 QVVEDDEDEDELTLYKAKHYIMLPVYTLQVVVAVATIKSVSEYTRKDGOLITPTPE 120
 OY 121 DEETGQORALSHSLNAIMISYVNTLLVLYKRCYKVIHAWLISSLLFFSFYI 180
 DB 121 DEETGQORALSHSLNAIMISYVNTLLVLYKRCYKVIHAWLISSLLFFSFYI 180
 OY 181 YLGEVFKRYTNVANDYITVALIWNLCVGMISIHMKGPLRLOQAYLIMISALMALVFIKY 240
 DB 181 YLGEVFKRYTNVANDYITVALIWNLCVGMISIHMKGPLRLOQAYLIMISALMALVFIKY 240
 OY 241 LPENTAMLIAYSYDLAVLCRPGPLMLVETAGERNETLEPALIYS 289
 DB 241 LPENTAMLIAYSYDLAVLCRPGPLMLVETAGERNETLEPALIYS 289

RESULT 6
 O9IUV3 PRELIMINARY; PRT; 448 AA.
 AC O9IUV3;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Presentinlin 2.
 GN PSEN2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-BREAST TUMOR;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC010403; AAH04043.1; -;
 DR MGP: MGI:109284; Psen2.
 DR InterPro: IPR001108; Presentinlin.
 DR Pfam: PF01080; Presentinlin; 1.
 SQ SEQUENCE 448 AA; 49964 MM; 2ED1DE7AFC3E0581 CRC64;


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Db 242 FIKYLEPWSAWIIGALISYIDLIAVLCRPGRLMLVETAOERNEDIFPALIYSSAMVMV 301
|||
Qy 297 NMAE-----DPEAQRVSKNSKYNASTRESODIYAENDDCGFSSEWEARQDSHLCPRS 353
|||
Db 302 GMAOSNPNDSAGERRS-----GGGVRTQGVSESHAP--- 335
|||
Qy 354 TPESRAAVQELSSSILAGEDEPEE-RGVKLGIDFIYSVLVGKASATASGDMNTIACFV 412
|||
Db 336 ----QAGRRQYS-----AEEDLEEDRGVKGIDFIYSVLVGKAAAT-GGDMNTIACFV 386
|||
Qy 413 AILGLCTLLLLAIFKKALPALPISITFGLVFPAATDLYVOPMDOLAFHOFYI 467
|||
Db 387 AILGLCTLLLLAIFKKALPALPISITFGLVFPAATDLYVOPMDOLAFHOFYI 441
|||
RESULT 9
ID Q8WS58 PRELIMINARY; PRT; 504 AA.
AC Q8WS58;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Presentlin.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
CX NCBI_TaxID=7739;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21590369; PubMed=11733140;
RA Martinez-Mir A., Canestro C., Gonzalez-Duarte R., Albalat R.;
RT "Characterization of the amphioxus presentlin gene in a high gene-
RT density genomic region illustrates duplication during the vertebrate
RT lineage."
RL Gene 279:157-164(2001).
DR EMBL; AF369891; AAL40416.1; JOINED.
DR Interpro: IPR000847; HTH_LYSR.
DR Interpro: IPR001108; Presentlin.
DR Pfam: PF01080; Presentlin; 1.
DR PROSITE: PRO1072; PRESENTLIN.
DR PROSITE: PS00044; HTH_LYSR_FAMILY; UNKNOMN.1.
SQ SEQUENCE 504 AA; 55443 MW; 9C3794D0302859B4 CRC64;

Query Match 57.3%; Score 1370; DB 5; Length 504;
Best Local Similarity 58.8%; Pred. No. 5.8e-106;
Matches 275; Conservative 56; Mismatches 101; Indels 36; Gaps 7;

Qy 27 RSONDNREORHNDRRSLGHPPLNSGRPOGNSRQVYODEDEDELTLKYGAKHYIMLF 86
|||
Db 46 RSQIQENTPGCADRRRG-----DGEDHGIHRH--EDDEEDTEMLTKGAKHYIMLF 98
|||
Qy 87 VPTLCMNVVAVATIKSVSYTRKQDLITPTEDTETVGORALHISINAAIMISIVVM 146
|||
Db 99 APVSLCMAVVAVATISSITFTYKNGYLITPHEEGASTASKVSGSLNCAIMVGVILVM 158
|||
Qy 147 TILLVLYKRYCYKYTAHMLISSLILFFSFYILGVEFKTYNAVDTYIVALLIMNLG 206
|||
Db 159 TFFLVLYKRYCYKYTHGMLISSLIMLFLFAYIYLGEVLAQYINPCYITLAIYMMNGF 218
|||
Qy 207 VVGMSTHMKGPLRLQOAVYIMISALMLVFKYLPENTAMILAVISYDLYAVALCRG 266
|||
Db 219 AVGMCHMKGPLRLQOAVYLVISALMLVFKYLPDWTWTWIIAISLYDLVAVALCRG 278
|||
Qy 267 PLRMLVETAOERNETLFPALIIYSSPMVLMVMAEGDPEAQRVSKNSKYNASTRES-- 324
|||
Db 279 PLKVLVETAOERNETLFPALIIYSSPMVLMVMAEGDPEAQRVSKNSKYNASTRES-- 338
|||
Qy 335 -QDTVAENDDCGFSSEWEARQ--DSHLCPRH-----TPESRAAVQELSSSILA-- 370
|||
Db 339 PAGAVGGEEGCGFDPMWNSRGFOPTRRPNRGNASDASVNSEDARQAQNINSLSPS 398
|||
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Qy 371 -----GEDEBRGVKLGIDFIYSVLVGKASATASGDMNTIACFVAILIGLC 419
|||
Db 399 GNOQOQOQMEDEDEEERGVKLGIDFIYSVLVKAS--SGDMNTIACFVAILIGLC 456
|||
Qy 420 LTLLLAIFKKALPALPISITFGLVFPAATDLYVOPMDOLAFHOFYI 467
|||
Db 457 LTLLLAIFKKALPALPISITFGLVFPAATDLYVOPMDOLAFHOFYI 504
|||
RESULT 10
ID Q9OX07 PRELIMINARY; PRT; 451 AA.
AC Q9OX07;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Presentlin 2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Korade Mirnes Z., Kerjanov S., Lovelock J., Corey S.J.;
RT "Cloning of chicken presentlins."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY043493; AAK95409.1; -.
DR Interpro: IPR001108; Presentlin.
DR Pfam: PF01080; Presentlin; 1.
SQ SEQUENCE 451 AA; 50496 MW; 534E6364C627E8B0 CRC64;

Query Match 57.2%; Score 1368.5; DB 13; Length 451;
Best Local Similarity 60.3%; Pred. No. 6.7e-106;
Matches 282; Conservative 46; Mismatches 75; Indels 65; Gaps 8;

Qy 3 ELPAPLSTFYQNAQMSDNHLSNTVRSQNDNREORHNDRRSLGHPPLNSGRPOGNSR-- 60
|||
Db 25 EEPVPSYQDQIQAQE-----TRAQHRRKQRT-----GSSNSP 58
|||
Qy 61 -QVVEQD-----EEDEDELTKYGAKHYIMLFVPTLCMNVVAVATIKSVSY 106
|||
Db 59 NNVADESDSDVYRRESALENEEDELTKYGAKHYIMLFVPTLCMNVVAVATIKSVSY 118
|||
Qy 107 TRKDQDLITPTEDTETVGORALHISINAAIMISIVVMITLVLYKRYCYKYTAHML 166
|||
Db 119 TEKNQDLITPTEDTETVGORALHISINAAIMISIVVMITLVLYKRYCYKYTHGWL 178
|||
Qy 167 IISLLILFFSFYILGVEFKTYNAVDTYIVALLIMNLGVVGMSTHMKGPLRLQOAVL 226
|||
Db 179 ILSFMLFLFYIYLGEVLTNYAMDYPIYILIMNFGAVGMIRIHMKGPLRLQOAVL 238
|||
Qy 227 IMISALMLVFKYLPENTAMILAVISYDLYAVALCRGPLRLVETAOERNETLFPAL 286
|||
Db 239 IMISALMLVFKYLPENTAMILAVISYDLYAVALCRGPLRLVETAOERNETLFPAL 298
|||
Qy 267 IYSSPMVLMVMAEGDPEAQRVSKNSKYNASTRESODIYAENDDCGFSSEWEARQDS 346
|||
Db 299 IYSSAMITVGNAK--PPTAARGOQOQAMADAD-BRENHSSYSHSD-----SQ 343
|||
Qy 347 HLGPRSTPESRAAVQELSSSILAGEDEPEERGVKLGIDFIYSVLVGKASATASGDMNT 406
|||
Db 344 ILDTSPAPSHPTILEM-----EEERGVKLGIDFIYSVLVGKAAATPSPGDMNT 395
|||
Qy 407 TIACFVAILIGLCITLLAIFKKALPALPISITFGLVFPAATDLYVQ 454
|||
Db 396 TLAXXVAILIGLCITLLAIFKKALPALPISITFGLVFPAATDLYVQ 443
|||
RESULT 11
ID Q8WS59 PRELIMINARY; PRT; 525 AA.
AC Q8WS59;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Presentlin.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
CX NCBI_TaxID=7739;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21590369; PubMed=11733140;
RA Martinez-Mir A., Canestro C., Gonzalez-Duarte R., Albalat R.;
RT "Characterization of the amphioxus presentlin gene in a high gene-
RT density genomic region illustrates duplication during the vertebrate
RT lineage."
RL Gene 279:157-164(2001).
DR EMBL; AF369891; AAL40416.1; JOINED.
DR Interpro: IPR000847; HTH_LYSR.
DR Interpro: IPR001108; Presentlin.
DR Pfam: PF01080; Presentlin; 1.
DR PROSITE: PRO1072; PRESENTLIN.
DR PROSITE: PS00044; HTH_LYSR_FAMILY; UNKNOMN.1.
SQ SEQUENCE 504 AA; 55443 MW; 9C3794D0302859B4 CRC64;
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AC O8MS59;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Presentlin.
 GN PS.
 OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
 OC Branchiostoma.
 OX NCBI_TaxID=7739;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21590369; PubMed=11733140;
 RA Martinez-Mar A., Canestro C., Gonzalez-Duarte R., Albalat R.;
 RT "Characterization of the amphioxus presentlin gene in a high gene-
 RT density genomic region illustrates duplication during the vertebrate
 RT lineage."
 RL Gene 279:157-164(2001).
 DR EMBL; AF369891; AAL0414.1; -.
 DR EMBL; AF369890; AAL0414.1; JOINED.
 DR InterPro; IPR000847; HTH_LYSR.
 DR InterPro; IPR001108; Presentlin.
 DR Pfam; PF01080; Presentlin; 1.
 DR PRINTS; PRO1072; Presentlin.
 DR PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
 DR PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
 SQ SEQUENCE 525 AA; 57598 MW; 2B14CF7A80F07DE CRC64;

Query Match 57.0%; Score 1362.5; DB 5; Length 525;
 Best Local Similarity 56.6%; Pred. No. 2.6e-105;
 Matches 277; Conservative 56; Mismatches 99; Indels 57; Gaps 8;

27 RSQNDNREQEHNDNRSLGHPPLNSGRPOGNSROVDEDEDEDELTLYGAKHYMLF 86
 DB 46 RSQNDNREQEHNDNRSLGHPPLNSGRPOGNSROVDEDEDEDELTLYGAKHYMLF 98
 DB 87 VVTCICMAYVAVATISITFTYTERKNGLYTPPHEGASTASKVSGSLANGALMVGILVM 146
 DB 99 AVVSICMAYVAVATISITFTYTERKNGLYTPPHEGASTASKVSGSLANGALMVGILVM 158
 DB 147 TLLVLLVLYKRCYKVIHAWLILISLLLEFFSFYILGEVFKTYNAVDYITVALLIMNLG 206
 DB 159 TVEVILVLYKRCYKVIHAWLILISLLLEFFSFYILGEVFKTYNAVDYITVALLIMNLG 218
 DB 207 VVGMTSIHKKGPLRLQOAVLIMISALMALVETIKYLPENTAMILLAVISYVDLVAALCPKG 266
 DB 219 AVGMCICHHKGPLRLQOAVLIMISALMALVETIKYLPENTAMILLAVISYVDLVAALCPKG 278
 DB 267 PLKMLVETQOEENETLFPALIVSSTMVWLVYMAEGDPEAQRVSKNSKYNALS----- 319
 DB 279 PLKMLVETQOEENETLFPALIVSSTMVWLVYMAEGDPEAQRVSKNSKYNALS----- 338
 DB 320 ---TERESQDT-----VAENDGCFSEEMEAQR--DSHLGPHR----- 352
 DB 339 FFLDNLNENGSTGDDADAPAPAGAVGGEBSGFGPDWMEBSGFGQTRPRPNNGNADAS 398
 DB 353 -STPESRAAVQELSSSIIA-----GEPDEERGVKLGIDTFYFVYLVGKASA 398
 DB 399 VASEPARQAQMLNSGRISPSGNQOOQOOMEDEDEDEEERGVKLGIDTFYFVYLVGKASA- 457
 DB 399 TASGMNTTIACTVAILIGLCTLLLAIFKRALPALPISITFGVLYATYLVLOPEMD 458
 DB 458 -SNGDMNTTIACTVAILIGLCTLLLAIFKRALPALPISITFGVLYATYLVLOPEMD 516
 DB 459 OLAFHOQFYI 467
 DB 517 ALASQOQVY 525

RESULT 12
 ID 09GU38 PRELIMINARY; PRT; 582 AA.
 AC 09GU38;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Presentlin.
 GN PS.
 OS Helix lucorum.
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylionmatophora;
 OC Helicidae; Helicidae; Helix.
 OX NCBI_TaxID=31229;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rogaev E.I., Riazanskaya N.N., Dvorianichkov G., Grigorenko A.P.,
 RA Tyurin O.;
 RT "Presentlin gene isolated from mollusk Helix lucorum";
 RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF197881; AAC28518.1; -.
 DR InterPro; IPR001108; Presentlin.
 DR Pfam; PF01080; Presentlin; 1.
 DR PRINTS; PRO1072; Presentlin.
 DR PROSITE; PRO1072; Presentlin.
 SQ SEQUENCE 582 AA; 63782 MW; 07934E7C452199F0 CRC64;

Query Match 52.0%; Score 1243.5; DB 5; Length 582;
 Best Local Similarity 48.1%; Pred. No. 2.5e-95;
 Matches 267; Conservative 73; Mismatches 108; Indels 107; Gaps 11;

9 SYFQNAQNSQEDNHLNTV-----RSQNDNREQEHNDNRSLGHPPLNS-----NGR 54
 DB 39 SYFQNAQNSQEDNHLNTV-----RSQNDNREQEHNDNRSLGHPPLNS-----NGR 97
 DB 55 PQGNSROYVDEDEDEDELTLYGAKHYMLFPVTLICMAYVAVATISITFTYTERKNGLY 114
 DB 98 PEGGN-----QEDDEE-TLLYGAKHYMLFPVTLICMAYVAVATISITFTYTERKNGLY 151
 DB 115 YTFPTEDETQVQARLHSLNAIMISVIVVMTLLVLYKRCYKVIHAWLILISLL 174
 DB 132 YTFPTEDETQVQARLHSLNAIMISVIVVMTLLVLYKRCYKVIHAWLILISLL 211
 DB 175 PFFSTIYGEVFKTYNAVDYITVALLIMNLGVGMSIHHKGPLRLQOAVLIMISALMA 234
 DB 212 PFFSTIYGEVFKTYNAVDYITVALLIMNLGVGMSIHHKGPLRLQOAVLIMISALMA 271
 DB 235 LVFITYLPENTAMILLAVISYVDLVAALCPKGPLMLVETQOEENETLFPALIVSSTMVW 294
 DB 272 LVFITYLPENTAMILLAVISYVDLVAALCPKGPLMLVETQOEENETLFPALIVSSTMVW 331
 DB 295 LVYMAEGDPEAQRVSKNSKYNALS-----SSILAGED----- 373
 DB 332 PVTMADDDGQSKKKQKKKGLKTGAQNSVYTPPLKDT--DDDGGFTEHVAANGTRQHS 389
 DB 348 LGPHRSTPESRAAVQEL-----SSILAGED----- 373
 DB 390 LTAQSDQSARNAVOAFGDMVQDKPRTDRNAVSHTTVYNTTSARVATRKDAGVESAVR 449
 DB 374 -----PEERGVKLGIDTFYFVYL 392
 DB 450 VAVDQROGAVYVANSRSQNSKTRPALQRRPLDSIDDDSEERGVKLGIDTFYFVYL 509
 DB 393 VGRASATASGDMNTTIACTVAILIGLCTLLLAIFKRALPALPISITFGVLYATYLV 452
 DB 510 VGRAS--SNGDMNTTIACTVAILIGLCTLLLAIFKRALPALPISITFGVLYATYLV 567
 DB 453 VQPMQDLAFHOQFYI 467
 DB 568 VQPMQDLAFHOQFYI 582

RESULT 13
 ID 091WK6 PRELIMINARY; PRT; 261 AA.
 AC 091WK6;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Similar to presentlin 1.


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GN PSEN1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EYE, AND RETINA;
RA Strausberg R.;
RL Submitted (Oct-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL, BC014744; AAI4744.1; -.
DR MGI; MGI:120217; Psen1.
DR InterPro: IPR001108; Psen11n.
DR Pfam: PF01080; Psen11n; 1.
SQ SEQUENCE 261 AA; 29849 MW; 16FB53FBE20EA4EB CRC64;

Query Match 51.1%; Score 1221; DB 11; Length 261;
Best Local Similarity 91.8%; Pred. No. 6,9e-94;
Matches 235; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

OY 1 MTELPAPLSYFQNAQMSQEDNHLSTNVRSONDRERQEHDRSLGHPRELSNGRQGNR 60
Db 1 MTELPAPLSYFQNAQMSQEDSHSSAIRSONDSQERQOHDRQDPPEPISNGRQGNR 60
OY 61 QVVEODEDEDELTLYGAKHVMLEFPVTLQMVVVVATIKSVSFYTRKQGLIYPTPE 120
Db 61 QVVEODEDEDELTLYGAKHVMLEFPVTLQMVVVVATIKSVSFYTRKQGLIYPTPE 120
OY 121 DTEWGORALHSILNAAIMISIVVMTLLVLYKRCYKVIHAWLIISLLLEFFSF 180
Db 121 DTEWGORALHSILNAAIMISIVVMTLLVLYKRCYKVIHAWLIISLLLEFFSF 180
OY 181 YGGEVFNKTVNAVDTYVALLLIMNGVGMISIHMKGPLRLOQAYLIMISALMALVF 240
Db 181 YGGEVFNKTVNAVDTYVALLLIMNGVGMISIHMKGPLRLOQAYLIMISALMALVF 240
OY 241 LPEWTAMLIAVISY 256
Db 241 LPEWTAMLIAVISY 256

RESULT 14
OY 096P32 PRELIMINARY; PRT; 390 AA.
AC 096P32:
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Psen11n 2 transcript variant 2 (Fragment).
GN PSEN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC xu Y., Hu X., Zhou Y., Peng X., Yuan J., Qiang B.;
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL, AF416718; AAL16812.1; -.
DR InterPro: IPR001108; Psen11n.
DR Pfam: PF01080; Psen11n; 1.
FT NON-TER 390
SQ SEQUENCE 390 AA; 43727 MW; A62C791CED9DCF8A CRC64;

Query Match 49.7%; Score 1188; DB 4; Length 390;
Best Local Similarity 62.0%; Pred. No. 6,4e-91;
Matches 253; Conservative 35; Mismatches 78; Indels 42; Gaps 8;
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Db 75 -----LEEEELTKGAKHVMLEFPVTLQMVVVVATIKSVFYEKNGQLIYPTFD 127
OY 122 TETVGORALHSILNAAIMISIVVMTLLVLYKRCYKVIHAWLIISLLLEFFSF 181
Db 128 TPVSGQRLNSVLLIMISIVVMTLLVLYKRCYKVIHAWLIISLLLEFFSF 187
OY 182 LGEVFNKTVNAVDTYVALLLIMNGVGMISIHMKGPLRLOQAYLIMISALMALVF 241
Db 188 LGEVFNKTVNAVDTYVALLLIMNGVGMISIHMKGPLRLOQAYLIMISALMALVF 247
OY 242 PWTAMLIAVISYVDLVAVLCPKGPLRLVETAEERNTLPPALISYSTMVLYMAAG 301
Db 248 PEMSAMVILGALISYVDLVAVLCPKGPLRLVETAEERNTLPPALISYSTMVLYMAAG 307
OY 302 DPEAQRVSKNKNYNAESTERESQDTVAENDDGGSEENEAQDSHLCGRSTPESRAV 361
Db 308 DPEAQRVSKNKNYNAESTERESQDTVAENDDGGSEENEAQDSHLCGRSTPESRAV 349
OY 362 OEISSILLAGEDPEERGVKLGDFYFVLYGKASATAGDMNTTIA 409
Db 350 EEL-----EEBERGAKLGJDELFTSYLVGKAKATGSDMNTTIA 390

RESULT 15
OY 09D616 PRELIMINARY; PRT; 332 AA.
AC 09D616:
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 0 day neonate head cDNA, RIKEN full-length enriched library,
clone:4833416A15, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=HEAD;
RL MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiava H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staubl F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schenbach C., Seya R., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL, AK014706; BAB29514.1; -.
DR InterPro: IPR001108; Psen11n.
DR Pfam: PF01080; Psen11n; 1.
DR PRINTS; PRO1072; Psen11n.
SQ SEQUENCE 332 AA; 37588 MW; 5728A699675A7D4D CRC64;

Query Match 39.8%; Score 952.5; DB 11; Length 332;
Best Local Similarity 72.0%; Pred. No. 2,3e-71;
Matches 190; Conservative 22; Mismatches 35; Indels 17; Gaps 3;
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Db      48  RTQSESEDEEDPDRYACSGAP-----GRPSG-----LEBELTLKYGANDVIML 91
OY      86  FVPTLCMVVATIKSVSFYTRKDGOLYTPTEDETFYGORALHSILNAIMISVIYV 145
      |||||||:||||||| ||| :||||||| ||| :||| |||||||
Db      92  FVPTLCMIVVATIKSVREYTEKNGOLYTPTEDETPSYGORLNSVLTLMISVIYV 151
OY      146  MTLVLVLYKRCYKVIAHMLISSLLEFESFTYLGVEYKTYNVAVDYITVALLIMNL 205
      ||||||| ||| :||| ||| :||| ||| :||| ||| :|||
Db      152  MTFELVLYKRCYKFIHGLIMSSLMLEFLFYIYLGVEYKTYNVAVDYPTFLAVWNE 211
OY      206  GYVGMISIHMKGPLRLOQAVLIMISALMALVFYKYLPEWTAWLILAVISYVDLAVLCPR 265
Db      212  GAVGMVCIHMKGPLVLOQAVLIVISALMALVFIKYLPEWSAWVILGAVISYVDLAVLCPR 271
OY      266  GPLRMLVETAQERNETLFPALIYS 289
      ||||||| ||| :||| ||| :||| ||| :|||
Db      272  GPLRMLVETAQERNETLFPALIYS 295

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Search completed: March 14, 2003, 20:08:58
 Job time : 70 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 19:14:13 ; Search time 38 Seconds
(without alignments)
1637.580 Million cell updates/sec

Title: US-09-689-159A-2

Perfect score: 2391

Sequence: 1 MTELPAPLSYFQNMASEDN.....ATDYLVQPFMDLAFHGFYI 467

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*

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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2387	99.8	467	17	AAW05733
2	2387	99.8	467	19	AAW23964
3	2387	99.8	467	19	AAW41430
4	2387	99.8	467	20	AAW24419
5	2387	99.8	467	20	AAV23897
6	2387	99.8	467	21	AAW07971
7	2387	99.8	467	22	AAE10798
8	2387	99.8	467	22	AAE05936
9	2387	99.8	467	22	AAE05466
10	2387	99.8	467	23	AAO18049

11	2387	99.8	467	23	AAU79416	Human presenilin-1
12	2387	99.8	467	23	AAE17051	Human mutant prese
13	2384	99.7	467	17	AAW05755	Presenilin-1-1 L28
14	2384	99.7	467	17	AAW05758	Presenilin-1-1 L39
15	2384	99.7	467	17	AAW05737	Presenilin-1-1 V82
16	2383	99.7	467	17	AAW05754	Presenilin-1-1 A28
17	2383	99.7	467	17	AAW05736	Presenilin-1-1 A79
18	2383	99.7	467	17	AAW05747	Presenilin-1-1 I23
19	2383	99.7	467	17	AAW05563	Presenilin-1-1 A26
20	2383	99.7	467	22	AAE05565	Human presenilin p
21	2382	99.6	467	17	AAW05738	Presenilin-1-1 V96
22	2382	99.6	467	17	AAW05739	Presenilin-1-1 Y11
23	2382	99.6	467	17	AAW05741	Presenilin-1-1 I14
24	2382	99.6	467	17	AAW05746	Presenilin-1-1 I21
25	2382	99.6	467	17	AAW05748	Presenilin-1-1 A24
26	2382	99.6	467	18	AAW27176	Human S182 gene, p
27	2381	99.6	467	17	AAW05753	Presenilin-1-1 E28
28	2381	99.6	467	17	AAW05757	Presenilin-1-1 G38
29	2381	99.6	467	17	AAW05740	Presenilin-1-1 M13
30	2381	99.6	467	17	AAW05742	Presenilin-1-1 M14
31	2380	99.5	467	17	AAW05744	Presenilin-1-1 L17
32	2380	99.5	467	19	AAW56770	Homo sapiens PS-1.
33	2380	99.5	467	22	AAE05564	Human presenilin p
34	2379	99.5	467	17	AAW05752	Presenilin-1-1 P26
35	2378	99.5	467	17	AAW05743	Presenilin-1-1 H16
36	2378	99.5	467	17	AAW05745	Presenilin-1-1 G20
37	2377	99.4	467	17	AAW05751	Presenilin-1-1 P26
38	2377	99.4	467	23	AAE17045	Human mutant prese
39	2376	99.4	467	17	AAW05759	Presenilin-1-1 C41
40	2375	99.3	467	23	AAW05750	Presenilin-1-1 C26
41	2375	99.3	467	23	AAE17046	Human mutant prese
42	2366	99.0	465	21	AAV51393	Human S182 protein
43	2366	99.0	467	18	AAW11839	Human early onset
44	2365	98.9	467	23	AAE17047	Human mutant prese
45	2361	98.7	463	17	AAW05734	Presenilin-1-2. H

ALIGNMENTS

RESULT 1	AAW05733	standard; Protein; 467 AA.
ID	AAW05733;	
AC	AAW05733;	
XX		
DT	23-JUL-1997 (first entry)	
XX		
DE	Presenilin-1-1.	
XX		
KW	Presenilin-1; human; hps1-1; hps1-2; PS-2; Integral membrane protein; AD;	
KW	familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;	
KW	depression; antibody; gene expression modulator; therapy.	
OS	Homo sapiens.	
XX		
PN	W09634099-A2.	
XX		
PD	31-OCT-1996.	
XX		
PF	29-APR-1996; 96WO-CA00263.	
XX		
PR	31-JUL-1995; 95US-0509359.	
PR	28-APR-1995; 95US-0431048.	
PR	28-JUN-1995; 95US-0496841.	
XX		
PA	(HSCR-) HSC RES & DEV LP.	
XX	(UTOR) UNIV TORONTO GOVERNING COUNCIL.	
PI	Fraser PE, Rommens JM, St George-Hyslop PH;	
XX		
DR	WPI; 1996-497631/49.	
DR	N-PSDB; AAT40028.	

FT Misc-difference 285 "Ala285Val mutation site (Claim 18)"
FT Misc-difference 286 "Leu286Val mutation site (Claim 18)"
FT Misc-difference 322 "Leu322Val mutation site (Claim 18)"
FT Misc-difference 392 "Leu392Val mutation site (Claim 18)"
FT Misc-difference 410 "Cys410Tyr mutation site (Claim 18)"
FT Misc-difference 79 "Ala79Xaa mutation site"
FT Misc-difference 82 "Val82Leu mutation site"
FT Misc-difference 96 "Val96Phe mutation site"
FT Misc-difference 115 "Tyr115His mutation site"
FT Misc-difference 139 "Met139Thr mutation site"
FT Misc-difference 139 "Met139Val mutation site"
FT Misc-difference 146 "Met146Val mutation site"
FT Misc-difference 163 "His163Arg mutation site"
FT Misc-difference 163 "His163Tyr mutation site"
FT Misc-difference 209 "Gly209Val mutation site"
FT Misc-difference 211 "Ile211Thr mutation site"
FT Misc-difference 231 "Ala231Thr mutation site"
FT Misc-difference 246 "Ala246Glu mutation site"
FT Misc-difference 291..319 "residue 291-319 deletion site"
FT Misc-difference 384 "Gly384Ala mutation site"
FT Misc-difference 26..29 "residue 26-29 deletion, resulting from alternative splicing"
XX WO9801549-A2.
XX 15-JAN-1998.
XX 04-JUL-1997: 97WO-CA00475.
XX 02-JAN-1997: 97US-0034590.
XX 05-JUL-1996: 96US-0021673.
XX 12-JUL-1996: 96US-0021700.
XX 08-NOV-1996: 96US-0029895.
XX (HSCR-) HSC RES & DEV SR.
XX (UTOR) UNIV TORONTO GOVERNING COUNCIL.
XX Fraser PE, Rommens JM, St George-Hyslop PH;
XX WPI: 1998-286355/25.
XX N-PSDB: AAV04666.
XX New isolated mutant presenilin-1 genes - useful for developing
XX products for use in detection, diagnosis and therapy of Alzheimer's
XX disease and for drug screening
XX Claim 1; Page 180-182; 238pp; English.
XX This polypeptide comprises human presenilin-1 (hpsl). Its amino
XX acid sequence was deduced from an isolated cDNA clone (see AAV04666).
XX Another hpsl sequence (see AAW23965) results from alternative
XX splicing of the hpsl mRNA transcript. A murine psi homologue (see

CC AAW23966) and a human presenilin-2 protein (see AAW23967) are also
CC provided. Mutations in the PS-1 and PS-2 genes are linked to the
CC development in humans of forms of familial Alzheimer's disease
CC (FAD) and may be causative of other disorders, e.g. cognitive,
CC intellectual, neurological or physiological disorders such as
CC cerebral haemorrhage, schizophrenia, depression, mental retardation
CC and epilepsy. Use of the nucleic acids and proteins comprising or
CC derived from the presenilins is made in screening and diagnosing
CC FAD, identifying and developing therapeutics for treatment of FAD,
CC and in producing cell lines and transgenic animals useful as models
CC of FAD. Methods for identifying substances that bind to, or
CC modulate the activity of a presenilin protein, and methods for
CC identifying substances that affect the interaction of a
CC presenilin-interacting protein with a presenilin protein are also
CC disclosed.
XX Sequence 467 AA:
SQ
Query Match 99.8%; Score 2387; DB 19; Length 467;
Best Local Similarity 99.8%; Pred. No. 4.5e-235;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTELPAPLSTYFQNAQMSQDNHLSNTVRSQNDNRERQEHNDRLSGHPPLSNGRQNSR 60
DB 1 MTELPAPLSTYFQNAQMSQDNHLSNTVRSQNDNRERQEHNDRLSGHPPLSNGRQNSR 60
QY 61 QVEDDEDEDELTKYAKKHVIMLFVPTVTCMVVYVATITSVSYTYTRKDGOLITPPT 120
DB 61 QVEDDEDEDELTKYAKKHVIMLFVPTVTCMVVYVATITSVSYTYTRKDGOLITPPT 120
QY 121 DTEYVGORALSHLNAALMISYIVVMTLLVLYRCYKYVHAWLISSLLLPFSFI 180
DB 121 DTEYVGORALSHLNAALMISYIVVMTLLVLYRCYKYVHAWLISSLLLPFSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLIMNLGVGMISIMHGKPLRQOAYLIMISALMALVFIRY 240
DB 181 YLGEVFKTYNVAVDYITVALLIMNLGVGMISIMHGKPLRQOAYLIMISALMALVFIRY 240
QY 241 LPETAWLILAVISYVDVAVLCRGPRLMLVETQENNELFPALITSSIMWLVNNAE 300
DB 241 LPETAWLILAVISYVDVAVLCRGPRLMLVETQENNELFPALITSSIMWLVNNAE 300
QY 301 GDPKQRRVSKNSKYNASTERESQDTVAENDDGFSEMEQRDSHLGPHRSTPESRAA 360
DB 301 GDPKQRRVSKNSKYNASTERESQDTVAENDDGFSEMEQRDSHLGPHRSTPESRAA 360
QY 361 VOELSSITLAGEDEPERGVKLGIDFIFYSVLVCKASATASGDMWTTIACFVAIIGLCL 420
DB 361 VOELSSITLAGEDEPERGVKLGIDFIFYSVLVCKASATASGDMWTTIACFVAIIGLCL 420
QY 421 TLLLAIRKKALPALPISITGVLVFPATDYLVPFMQLAFHORYI 467
DB 421 TLLLAIRKKALPALPISITGVLVFPATDYLVPFMQLAFHORYI 467
RESULT 3
AAW41430
ID AAW41430 standard; Protein: 467 AA.
AC AAW41430;
DT 04-JUN-1998 (first entry)
XX PSI/467 protein.
XX Presenilin peptide; PSI/429; immunogen; immune response; PSI gene;
XX Alzheimer's disease; mitochondrial pathology; neurodegeneration;
XX apoptosis; PSI/467.
XX Homo sapiens.
XX OS
XX PN W09746678-A1.

PD 11-DEC-1997.
XX
XX 03-JUN-1997; 97WO-0509222.
XX
XX 18-JUL-1996; 96US-0683315.
PR 06-JUN-1996; 96US-0659296.
XX
XX (FARB) BAYER CORP.
PI Chisholm JC, Davis-JN, Drache B;
XX WPI: 1998-042186/04.
DR N-PSDB: AAY17358.
XX
PT DNA encoding presenilin peptide PSI/429 and its analogues - useful
XX for diagnosis and treatment of Alzheimer's disease
PS Claim 7; Fig 2; 77pp; English.

CC This sequence is the PSI/467 presenilin peptide. This sequence is
CC specifically stated as not being in the nucleic acid of the invention,
CC which encodes the PSI/429 presenilin peptide PSI/429 (II). Cells
CC transformed with the DNA are used to produce recombinant (II) and
CC analogues, useful e.g. as immunogens for generating an immune response
CC against PSI/429. (II) is a new product of the PSI gene, mutations in
CC which cause Alzheimer's disease (AD). The nucleic acids are generally
CC useful as probes for detection and quantification of PSI/429,
CC particularly for diagnosis of AD, especially the target sequences that
CC hybridise with probes are isolated for sequencing. Antibodies (Ab) can
CC also be diagnosed at the protein level using Ab as immunoassay reagents.
CC Ab can also be used to identify epitopes and for affinity purification of
CC peptides. Antisense nucleic acid may also be used to regulate expression
CC of the PSI/429 gene, and both nucleic acids and peptides are useful as
CC size markers in electrophoresis, chromatography etc. The transgenic
CC animals are used as models for AD, e.g. for testing drugs. Regulators of
CC the PSI/429 gene or polypeptide can be used to treat e.g. AD or diseases
CC involving mitochondrial pathology, apoptosis and neurodegeneration.
CC Typical regulators are antisense sequences, ribozymes, aptamers,
CC synthetic or natural compounds. (II) may also be used to target other
CC coding sequences to particular cellular locations.

XX Sequence 467 AA:

Query Match 99.8%; Score 2387; DB 19; Length 467;
Best Local Similarity 99.8%; Pred. No. 4.5e-235;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFONAOSEDNHLSNTVRSQNDNREOHNDRLSLGHPPLSGRPOGNSR 60
DB 1 MTELPAPLSYFONAOSEDNHLSNTVRSQNDNREOHNDRLSLGHPPLSGRPOGNSR 60
QY 61 QVEODEEEDDELTLKYGAKHIVMLFVPTLCMVVVAVATIKVSFTRKDGOLITPTE 120
DB 61 QVEODEEEDDELTLKYGAKHIVMLFVPTLCMVVVAVATIKVSFTRKDGOLITPTE 120
QY 121 DRETVGQRAHLSILNAIMISIVYVMTLLVLYKYRCYKVIHAWLISLLLEFFSPT 180
DB 121 DRETVGQRAHLSILNAIMISIVYVMTLLVLYKYRCYKVIHAWLISLLLEFFSPT 180
QY 121 DRETVGQRAHLSILNAIMISIVYVMTLLVLYKYRCYKVIHAWLISLLLEFFSPT 180
DB 121 DRETVGQRAHLSILNAIMISIVYVMTLLVLYKYRCYKVIHAWLISLLLEFFSPT 180
QY 181 YGGEVFKTYNNAVDTYVALILMNLGVGMISIHMKGPLRLOOAYILMISALMALVFIKY 240
DB 181 YGGEVFKTYNNAVDTYVALILMNLGVGMISIHMKGPLRLOOAYILMISALMALVFIKY 240
QY 241 LPEWPAWLILVAISYDVAVALCPKGPLMLVETAOERNETLFPALISSTVWLVNMAE 300
DB 241 LPEWPAWLILVAISYDVAVALCPKGPLMLVETAOERNETLFPALISSTVWLVNMAE 300
QY 301 GDPPEAQRVRSKSKYNAESTERESODTVAENDGGFSEEMEAQDSHLGPHRSTPESRAA 360
DB 301 GDPPEAQRVRSKSKYNAESTERESODTVAENDGGFSEEMEAQDSHLGPHRSTPESRAA 360
QY 361 VOELSSSILAGDPBERGVKLGDFIFYSVLVGKASATASCDMNTTACFAVAILIGLCL 420
DB 361 VOELSSSILAGDPBERGVKLGDFIFYSVLVGKASATASCDMNTTACFAVAILIGLCL 420

DB 361 VOELSSSILAGDPBERGVKLGDFIFYSVLVGKASATASCDMNTTACFAVAILIGLCL 420
QY 421 TLLLAIFKKALPALPISTFGLVFFATDYLVPFMDLAFHORYI 467
DB 421 TLLLAIFKKALPALPISTFGLVFFATDYLVPFMDLAFHORYI 467

RESULT 4
AAY24419
ID AAY24419 standard; Protein; 467 AA.

AC AAY24419;

DT 23-SEP-1999 (first entry)

DE Human presenilin-1.

XX Presentin-1; mutation; gene mutant animal; Alzheimer's disease.

OS Homo sapiens.

XX WO934670-A1.

PN 15-JUL-1999.

XX 07-JAN-1999; 99WO-JP00015.

XX 08-JAN-1998; 98JP-0002191.

XX (DAUC) DAICHI PHARM CO LTD.

PI Takeda J, Takeda M;

XX WPI: 1999-430307/36.

DR N-PSDB: AAX90184.

PT Mutant presenilin-1 gene-introduced animals, useful as model animals
XX for study of Alzheimer's diseases in human and screening substances
XX for prevention and/or treatment of the diseases

PS Disclosure: Page 51-52; 64pp; Japanese.

XX The present invention describes a gene mutant animal having a non-human
CC mutant presenilin gene. The mutant presenilin gene causes amino acid
CC substitutions at 1 or more positions of 79, 82, 96, 115, 120, 135, 139,
CC 143, 146, 163, 209, 213, 231, 235, 246, 250, 260, 263, 264, 267, 269,
CC 280, 285, 286, 290, 318, 384, 392, 410, 426 and 436, with corresponding
CC N-terminals being e.g. A79V, V82L, A426 and P436S, particularly by
CC replacing isoleucine of position 213 by another amino-acid especially
CC threonine. The gene mutant animals e.g. mice can be used as model
CC animals for the study of human Alzheimer's diseases and to screen and
CC evaluate substances as candidates for prevention and/or therapy of
CC Alzheimer's diseases in patients. They can over-produce amyloid
CC beta protein by the presenilin-1 gene to cause nerve cell death or
CC peeling off in the hippocampus earlier. Such animals are being
CC pathologically close to human patients with Alzheimer's diseases. The
CC present sequence represents human presenilin-1, as given in the present
XX invention.

XX Sequence 467 AA:

Query Match 99.8%; Score 2387; DB 20; Length 467;
Best Local Similarity 99.8%; Pred. No. 4.5e-235;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFONAOSEDNHLSNTVRSQNDNREOHNDRLSLGHPPLSGRPOGNSR 60

DB 1 MTELPAPLSYFONAOSEDNHLSNTVRSQNDNREOHNDRLSLGHPPLSGRPOGNSR 60

QY 61 QVEODEEEDDELTLKYGAKHIVMLFVPTLCMVVVAVATIKVSFTRKDGOLITPTE 120
DB 61 QVEODEEEDDELTLKYGAKHIVMLFVPTLCMVVVAVATIKVSFTRKDGOLITPTE 120

QY 121 DTEVGQRALHSILNAIMISYIVVMTLLVLYKRCYKVIHAWLISSLLFFFSFI 180
 DB 121 DTEVGQRALHSILNAIMISYIVVMTLLVLYKRCYKVIHAWLISSLLFFFSFI 180
 QY 181 YLGEVFKTYNVAVDYITVALIMNIGVGMISIHMKGPLRLOQAVYIMISALMALVFIRY 240
 DB 181 YLGEVFKTYNVAVDYITVALIMNIGVGMISIHMKGPLRLOQAVYIMISALMALVFIRY 240
 QY 241 LPEWTAMLLAVISYVDLAVLCPPKPLMLVETAOERNETLFPALISSTWMLVNMME 300
 DB 241 LPEWTAMLLAVISYVDLAVLCPPKPLMLVETAOERNETLFPALISSTWMLVNMME 300
 QY 301 GPEAQRVSKSKYNAESTERESODTVAENDGCFSEEMEAQRDHLGPHRSTPESRAA 360
 DB 301 GPEAQRVSKSKYNAESTERESODTVAENDGCFSEEMEAQRDHLGPHRSTPESRAA 360
 QY 361 VOELSSSILAGEDPEERGVKLGDFIEFYSVLGKASATASGDMNTTICFVAIILGLCL 420
 DB 361 VOELSSSILAGEDPEERGVKLGDFIEFYSVLGKASATASGDMNTTICFVAIILGLCL 420
 QY 421 TLLLLAIFKKALPALPISITFGIVFYFATDYLVQPMQLAFHQFYI 467
 DB 421 TLLLLAIFKKALPALPISITFGIVFYFATDYLVQPMQLAFHQFYI 467

RESULT 5

AAY23897
 ID AAY23897 standard; protein; 467 AA.

XX AAY23897;
 XX

DT 27-SEP-1999 (first entry)
 XX

DE Amino acid sequence of the wild type human presenilin 1 (PS1) protein.
 XX

KM Human; presenilin 1; PS1; presenilin-binding protein; interacting domain;
 KM presenilin allele; Alzheimer's disease; senile dementia;
 KM psychiatric disease; schizophrenia; depression; neurological disease;
 KM stroke; cerebral haemorrhage.
 XX

OS Homo sapiens.
 XX

PN W09935501-A1.
 XX

PD 15-JUL-1999.
 XX

PF 08-JAN-1999; 99WO-CA00018.
 XX

PR 09-JAN-1998; 98US-0070948.
 XX

PA (UNOR) UNIV TORONTO GOVERNING COUNCIL.
 XX

PI Fraser PE, St George-Hyslop PH.
 XX

DR WPI; 1999-419410/35.
 XX

PT Identifying substances that alter presenilin interactions, useful
 PT for screening individuals for presenilin alleles associated with
 PT Alzheimer's disease - useful for diagnosis of Alzheimer's disease
 XX

PS Disclosure: Page 34-36; 40pp; English.
 XX

CC The present sequence represents wild type human presenilin 1 (PS1)
 CC protein. The specification describes a method for identifying substances
 CC that alter the interaction of a presenilin with a presenilin-binding
 CC protein. The method comprises contacting the interacting domain of a
 CC presenilin protein to a presenilin-binding protein in the presence of
 CC a test substance, and measuring the interaction of the presenilin and
 CC the presenilin-binding protein. The method can be used to screen
 CC individuals for presenilin alleles associated with Alzheimer's disease
 CC and related disorders, such as senile dementia's, psychiatric diseases
 CC such as schizophrenia and depression, and neurological disease, such as
 CC stroke and cerebral haemorrhage.

XX SQ Sequence 467 AA:

Query Match 99.8%; Score 2387; DB 20; Length 467;
 Best Local Similarity 99.8%; Pred. No. 4,5e-235;
 Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLISYFQNAQSEDNHLSNTVRSQNDREHNDRLSGHPEPLSGRPGNSR 60
 DB 1 MTELPAPLISYFQNAQSEDNHLSNTVRSQNDREHNDRLSGHPEPLSGRPGNSR 60
 QY 61 QVVEODEEEDDELTLKYGAKHYIMLFVPTLCMVVAVATIKSYFTRKQGLIYPTPE 120
 DB 61 QVVEODEEEDDELTLKYGAKHYIMLFVPTLCMVVAVATIKSYFTRKQGLIYPTPE 120
 QY 121 DTEVGQRALHSILNAIMISYIVVMTLLVLYKRCYKVIHAWLISSLLFFFSFI 180
 DB 121 DTEVGQRALHSILNAIMISYIVVMTLLVLYKRCYKVIHAWLISSLLFFFSFI 180
 QY 181 YLGEVFKTYNVAVDYITVALIMNIGVGMISIHMKGPLRLOQAVYIMISALMALVFIRY 240
 DB 181 YLGEVFKTYNVAVDYITVALIMNIGVGMISIHMKGPLRLOQAVYIMISALMALVFIRY 240
 QY 241 LPEWTAMLLAVISYVDLAVLCPPKPLMLVETAOERNETLFPALISSTWMLVNMME 300
 DB 241 LPEWTAMLLAVISYVDLAVLCPPKPLMLVETAOERNETLFPALISSTWMLVNMME 300
 QY 301 GPEAQRVSKSKYNAESTERESODTVAENDGCFSEEMEAQRDHLGPHRSTPESRAA 360
 DB 301 GPEAQRVSKSKYNAESTERESODTVAENDGCFSEEMEAQRDHLGPHRSTPESRAA 360
 QY 361 VOELSSSILAGEDPEERGVKLGDFIEFYSVLGKASATASGDMNTTICFVAIILGLCL 420
 DB 361 VOELSSSILAGEDPEERGVKLGDFIEFYSVLGKASATASGDMNTTICFVAIILGLCL 420
 QY 421 TLLLLAIFKKALPALPISITFGIVFYFATDYLVQPMQLAFHQFYI 467
 DB 421 TLLLLAIFKKALPALPISITFGIVFYFATDYLVQPMQLAFHQFYI 467

RESULT 6

AAB07971
 ID AAB07971 standard; protein; 467 AA.

XX AAB07971;
 XX

DT 14-NOV-2000 (first entry)
 XX

DE Amino acid sequence of human presenilin I polypeptide.
 XX

KM Human; presenilin; PS1; PS2; nerve cell growth; nerve damage; hnpRAP;
 KM neural plakophilin related armadillo protein; Alzheimer's disease;
 KM Parkinson's disease; amyotrophic lateral sclerosis; ALS; stroke;
 KM multiple sclerosis; ischemia; stroke; neural paropathy; sciatic crush;
 KM motor neuron disease; peripheral neuropathy; neuropathy; diabetes;
 KM spinal cord injury; facial nerve crush.
 XX

OS Homo sapiens.
 XX

PN W0200047615-A2.
 XX

PD 17-NOV-2000.
 XX

PF 11-FEB-2000; 2000WO-CA00126.
 XX

PR 12-FEB-1999; 99US-0119835.
 XX

PA (UNOR) UNIV TORONTO GOVERNING COUNCIL.
 XX

PI St George-Hyslop PH, Fraser PE;
 XX

DR WPI; 2000-524531/47.
 XX

PT Stimulation of nerve cell growth using human Neural plakophilin Related
PT Armidillo Protein (hnpRap) polypeptide, useful for the treatment of
PT diseases such as Alzheimer's, Parkinson's, and stroke
XX
PS Disclosure: Page 19-20; 33pp: English.
XX
CC The present sequence represents a human presenilin 1 (PS1) polypeptide.
CC Human Neural Plakophilin Related Armidillo Protein (hnpRap) polypeptide
CC is known to interact with PS1 and PS2. The specification describes a
CC method for stimulating the growth of nerve cells, comprising contacting
CC them with hnpRap. The hnpRap polypeptide and polynucleotide are useful
CC for treating nerve damage caused by a variety of diseases or physical
CC trauma, including Alzheimer's disease, Parkinson's disease, amyotrophic
CC lateral sclerosis (ALS), multiple sclerosis, stroke, ischemia associated
CC with stroke, neural paropathy, motor neuron diseases, sciatic crush,
CC peripheral neuropathy, neuropathy associated with diabetes, spinal cord
CC injuries and facial nerve crush.
XX
SQ Sequence 467 AA:

Query Match 99.8%; Score 2387; DB 21; Length 467;
Best Local Similarity 99.8%; Pred. No. 4.5e-235;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSTFQNAQSEDNHLSNTVRSQNDNREOHNDRLSGHPEPLSNCRPOGNSR 60
DB 1 MTELPAPLSTFQNAQSEDNHLSNTVRSQNDNREOHNDRLSGHPEPLSNCRPOGNSR 60
QY 61 QVVEODEEEDDELTKYGAKHVMLEFVPVTLQVNVVATIKSVSEYTRKDGOLITPPE 120
DB 61 QVVEODEEEDDELTKYGAKHVMLEFVPVTLQVNVVATIKSVSEYTRKDGOLITPPE 120
QY 121 DFTVQGRALHSILNAINMISIVVMTILLVLYKRCYKVIHAWLIISSLLFFESFI 180
DB 121 DFTVQGRALHSILNAINMISIVVMTILLVLYKRCYKVIHAWLIISSLLFFESFI 180
QY 181 YLGEVEKTYNVAVDYITVALLINWLGVMGSIHMKGPRLQOAYILMSALMALVFIKY 240
DB 181 YLGEVEKTYNVAVDYITVALLINWLGVMGSIHMKGPRLQOAYILMSALMALVFIKY 240
QY 241 LPMTAMLILAVISYDVAVALCPKGPLRLVETAOERNETLFPALITYSTWMLVNMME 300
DB 241 LPMTAMLILAVISYDVAVALCPKGPLRLVETAOERNETLFPALITYSTWMLVNMME 300
QY 301 GDEPAQRVSKNSKYNAAESTERESQDTVAENDDGFSEMEARQDSHLGPHRSTPESRAA 360
DB 301 GDEPAQRVSKNSKYNAAESTERESQDTVAENDDGFSEMEARQDSHLGPHRSTPESRAA 360
QY 361 VOELSSIIAGDEPBERGVKLGIDFTIFSYLVGKASATASGDMNTTACFAVAILIGLCL 420
DB 361 VOELSSIIAGDEPBERGVKLGIDFTIFSYLVGKASATASGDMNTTACFAVAILIGLCL 420
QY 421 TLLLLAIFKKALPALPISITFGLVFEFATDYLQPFMDQLAFHOFTYI 467
DB 421 TLLLLAIFKKALPALPISITFGLVFEFATDYLQPFMDQLAFHOFTYI 467

RESULT 7
ID AAE10798 standard; protein; 467 AA.
AC AAE10798;
XX
DE 18-DEC-2001 (first entry)
XX
DE Human presenilin-1 (PS-1) protein.
XX
KW Human; catenin p120; presenilin-1; PS-1; neuroprotective; gene therapy;
KW neurodegenerative disease; Alzheimer's disease; nootropic; propylaxis;
KW neuronal disorder; cognitive disorder.
XX
OS Homo sapiens.
XX

PN WO200167097-A2.
XX
PD 13-SEP-2001.
XX
PF 09-MAR-2001; 2001MO-GB01059.
XX
PR 10-MAR-2000; 2000GB-0005895.
XX
PA (GLAXO) GLAXO GROUP LTD.
XX
PI Hale RS, Rowley A, Blackstock W;
XX
DR WPI; 2001-589954/66.
XX
DR N-PSDB; AAD18120.
XX
PT Identifying presenilin or catenin p120 activity modulator useful for
PT modulating presenilin-catenin p120 interaction and thus for treating
PT cognitive disorder e.g., Alzheimer's disease comprises enhancing
PT cognitive function
XX
PS Example 1; Page 41-42; 48pp: English.
XX

CC The invention relates to a method for identifying modulators of
CC presenilin and catenin p120. Modulators of catenin p120 and presenilin
CC are useful for the treatment and prophylaxis of disorders that is
CC responsive to modulation of presenilin/catenin p120 activity. In
CC particular, neuronal disorders such as cognitive disorders and
CC neurodegenerative diseases such as Alzheimer's disease. Catenin p120 DNAs
CC are useful for identifying mutations in catenin p120 genes.
CC Identification of such mutations assist in the diagnosis of or
CC susceptibility to Alzheimer's or other conditions associated with
CC presenilin and in assessing the physiology of such disorders. Catenin
CC p120 DNAs are also used in hybridisation studies to monitor expression of
CC expression. The present sequence is human presenilin-1 (PS-1) protein.
XX
SQ Sequence 467 AA:

Query Match 99.8%; Score 2387; DB 22; Length 467;
Best Local Similarity 99.8%; Pred. No. 4.5e-235;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSTFQNAQSEDNHLSNTVRSQNDNREOHNDRLSGHPEPLSNCRPOGNSR 60
DB 1 MTELPAPLSTFQNAQSEDNHLSNTVRSQNDNREOHNDRLSGHPEPLSNCRPOGNSR 60
QY 61 QVVEODEEEDDELTKYGAKHVMLEFVPVTLQVNVVATIKSVSEYTRKDGOLITPPE 120
DB 61 QVVEODEEEDDELTKYGAKHVMLEFVPVTLQVNVVATIKSVSEYTRKDGOLITPPE 120
QY 121 DFTVQGRALHSILNAINMISIVVMTILLVLYKRCYKVIHAWLIISSLLFFESFI 180
DB 121 DFTVQGRALHSILNAINMISIVVMTILLVLYKRCYKVIHAWLIISSLLFFESFI 180
QY 181 YLGEVEKTYNVAVDYITVALLINWLGVMGSIHMKGPRLQOAYILMSALMALVFIKY 240
DB 181 YLGEVEKTYNVAVDYITVALLINWLGVMGSIHMKGPRLQOAYILMSALMALVFIKY 240
QY 241 LPMTAMLILAVISYDVAVALCPKGPLRLVETAOERNETLFPALITYSTWMLVNMME 300
DB 241 LPMTAMLILAVISYDVAVALCPKGPLRLVETAOERNETLFPALITYSTWMLVNMME 300
QY 301 GDEPAQRVSKNSKYNAAESTERESQDTVAENDDGFSEMEARQDSHLGPHRSTPESRAA 360
DB 301 GDEPAQRVSKNSKYNAAESTERESQDTVAENDDGFSEMEARQDSHLGPHRSTPESRAA 360
QY 361 VOELSSIIAGDEPBERGVKLGIDFTIFSYLVGKASATASGDMNTTACFAVAILIGLCL 420
DB 361 VOELSSIIAGDEPBERGVKLGIDFTIFSYLVGKASATASGDMNTTACFAVAILIGLCL 420
QY 421 TLLLLAIFKKALPALPISITFGLVFEFATDYLQPFMDQLAFHOFTYI 467
DB 421 TLLLLAIFKKALPALPISITFGLVFEFATDYLQPFMDQLAFHOFTYI 467

RESULT 8
AAC63936
ID AAC63936 standard; Protein: 467 AA.
AAC63936;
AC AAG63936;
XX
XX
XX 29-OCT-2001 (first entry)
DE Amino acid sequence of human presenilin 1.
XX
XX KIAA0253; presenilin; Alzheimer's disease.
OS Homo-sapiens.
XX
XX WO200167109-A1.
XX
XX 13-SEP-2001.
XX
XX 09-MAR-2001; 2001WO-GB01057.
XX
XX 10-MAR-2000; 2000GB-0005894.
XX
XX (GLAX) GLAXO GROUP LTD.
XX
XX Hale RS, Rowley A, Blackstock W;
XX
XX WPI: 2001-522960/57.
XX
XX N-PSDB: AAH74993.
XX
XX
XX Identifying a modulator of presenilin function by determining the
PT ability of presenilin to bind to a KIAA0253 polypeptide in the presence
PT and absence of a test compound, useful in the treatment or prophylaxis
PT of Alzheimer's disease -
XX
XX Disclosure: Page 40-41; 48pp; English.
XX
XX The present sequence represents human presenilin 1. KIAA0253 binds to
CC presenilin. The specification describes a method of identifying a
CC modulator of presenilin function or KIAA0253 function. The method
CC comprises determining presenilin activity or KIAA0253 activity
CC in the presence and absence of a test compound, where presenilin
CC activity is determined by its ability to bind to KIAA0253. A modulator
CC of presenilin or KIAA0253 polypeptide is useful in the manufacture of
CC a medicament for the treatment or prophylaxis of Alzheimer's disease.
CC The KIAA0253 polynucleotide and KIAA0253 polypeptide are useful in the
CC treatment, prophylaxis or diagnosis of Alzheimer's disease.
XX
XX
SQ Sequence 467 AA;
Query Match 99.8%; Score 2387; DB 22; Length 467;
Best Local Similarity 99.8%; Pred. No. 4,56-235;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTELPAPSTYRONQMSEDNHLSNTRVRSQNDNREOHNDNRSLGHPPLSLGRPOGNSR 60
DB 1 MTELPAPSTYRONQMSEDNHLSNTRVRSQNDNREOHNDNRSLGHPPLSLGRPOGNSR 60
QY 61 QVVEDEDEDELTKYAKAHVIMLFVPTLCMVVAVATIKSVSPYTRKDKQLITPTE 120
DB 61 QVVEDEDEDELTKYAKAHVIMLFVPTLCMVVAVATIKSVSPYTRKDKQLITPTE 120
QY 121 DTEYGGQALHSILMAIMISIVYVMTLLVLYKRCYKVIHAWLITSSLLFFESFI 180
DB 121 DTEYGGQALHSILMAIMISIVYVMTLLVLYKRCYKVIHAWLITSSLLFFESFI 180
QY 181 YLGEVFKYNAVDITVALLIMNGVVMISIHKKGPLRLQQAALMISALMAVFKY 240
DB 181 YLGEVFKYNAVDITVALLIMNGVVMISIHKKGPLRLQQAALMISALMAVFKY 240
QY 241 LPEWTAMLIAVISYVDLVAVLCPRGLRMLETVAQERNETLFPALISSTVMVLVNAE 300
DB 241 LPEWTAMLIAVISYVDLVAVLCPRGLRMLETVAQERNETLFPALISSTVMVLVNAE 300

DB 241 LPEWTAMLIAVISYVDLVAVLCPRGLRMLETVAQERNETLFPALISSTVMVLVNAE 300
QY 301 GDPAQRVRVSKNSKYNASTERESODTYAENDDGFSEEMPAQRSHLGPHRSTPESRAA 360
DB 301 GDPAQRVRVSKNSKYNASTERESODTYAENDDGFSEEMPAQRSHLGPHRSTPESRAA 360
QY 361 VOELSSSILAGEDPEPERGVKGLGDFIFYSVLVCKASATASGDMWTITACFAILIGLCL 420
DB 361 VOELSSSILAGEDPEPERGVKGLGDFIFYSVLVCKASATASGDMWTITACFAILIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGLVFFYFATDYLVOPFMDQLAFHOFYI 467
DB 421 TLLLAIFKKALPALPISITFGLVFFYFATDYLVOPFMDQLAFHOFYI 467
RESULT 9
AAE05466
ID AAE05466 standard; Protein: 467 AA.
XX
XX AAE05466;
AC
XX
XX 24-SEP-2001 (first entry)
XX
XX Human presenilin (PS1) protein.
XX
XX Human: Par-4; presenilin; PS1; neuroprotective; nuclear factor kappa B;
XX NF-kappa B; neuronal degeneration; spinal muscular atrophy; paralysis;
XX peripheral neuropathy; motorneuron disorder; neurodegenerative disorder;
XX Parkinson's disease; Meniere's disease; multiple sclerosis; Bell's palsy;
XX Huntington's chorea; Down's syndrome; amyotrophic lateral sclerosis; ALS;
XX nerve deafness; Alzheimer's disease; epilepsy.
XX
XX Homo-sapiens.
XX
XX WO200151671-A2.
XX
XX 19-JUL-2001.
XX
XX 08-JAN-2001; 2001WO-US00526.
XX
XX 10-JAN-2000; 2000US-0175200.
XX
XX 04-JAN-2001; 2001US-0754949.
XX
XX (SCIO-) SCIOS INC.
XX
XX McCarthy J, Cordell B;
XX
XX WPI: 2001-451872/48.
XX
XX N-PSDB: AAE05466.
XX
XX Identifying inhibitors of neuronal degeneration useful for treating
PT e.g. Alzheimer's disease, by determining the ability of a compound to
PT induce nuclear factor kappa B activation, with the involvement of
PT presenilin or Par-4 -
XX
XX
PS Claim 4; Page 60-61; 66pp; English.
XX
XX The invention relates to human Par-4 protein, presenilin protein (PS1
XX and PS2) and their corresponding DNA molecules. The invention also
XX relates to a method for identifying inhibitors of neuronal degeneration,
XX comprising cotransfecting eukaryotic host cells expressing presenilin
XX (PS), with a Par-4 DNA, and an NF-kappa B dependent reporter construct,
XX exposing the cotransfected cells to a candidate molecule and monitoring
XX the ability of the candidate molecule to induce NF-kappa B activation.
XX Presenilin proteins participates in nuclear factor kappa B (NF-kappa B)
XX signalling and activation. The inhibitors of neuronal degeneration
XX are useful for treating neurodegenerative disorders such as Alzheimer's
XX disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's
XX chorea, Down's syndrome, nerve deafness, Meniere's disease and also for
XX treating peripheral neuropathies, motorneuron disorders such as
XX amyotrophic lateral sclerosis (ALS), Bell's palsy and various conditions
XX involving spinal muscular atrophy and paralysis. The present sequence
XX is human presenilin (PS1) protein.

```
xx Sequence 467 AA:
SQ
Query Match 99.8%; Score 2387; DB 22; Length 467;
Best Local Similarity 99.8%; Pred. No. 4.5e-235;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTELPAPLSYFQNAQMSSEDNHLSNTVRSQNDNERQEHNDRLSLGHPPLSNRPOGNSR 60
Db 1 MTELPAPLSYFQNAQMSSEDNHLSNTVRSQNDNERQEHNDRLSLGHPPLSNRPOGNSR 60
QY 61 QVVEODEEEDDELTKYGAHVIMLEVPVTLCAVVVVAATIKVSFETRKDGQLIYPTFE 120
Db 61 QVVEODEEEDDELTKYGAHVIMLEVPVTLCAVVVVAATIKVSFETRKDGQLIYPTFE 120
QY 121 DTEVVGORALHSLTNAIMISVIVMTILVLYKYRCYKVHIAWLISLLFFFSFI 180
Db 121 DTEVVGORALHSLTNAIMISVIVMTILVLYKYRCYKVHIAWLISLLFFFSFI 180
QY 181 YLGEVEKTYNAVDYITVALLIWNLGVMISIMHGKPLRLQOAYLIMISALMALVFIKY 240
Db 181 YLGEVEKTYNAVDYITVALLIWNLGVMISIMHGKPLRLQOAYLIMISALMALVFIKY 240
QY 241 LPETWAMLILAVISYDVAVLCRKPRLMLETQAERNETLPPALISSTWVLMNMAE 300
Db 241 LPETWAMLILAVISYDVAVLCRKPRLMLETQAERNETLPPALISSTWVLMNMAE 300
QY 301 GDEPAQRVSKNSKYNAESTERESODTVAENDDGFSEMEAROSHLGPHRSTPESRAA 360
Db 301 GDEPAQRVSKNSKYNAESTERESODTVAENDDGFSEMEAROSHLGPHRSTPESRAA 360
QY 361 VOELSSSIILAGEDPEERGVKLGDFIFYSVLVGKASATASGDMNTTACFAAILIGLCL 420
Db 361 VOELSSSIILAGEDPEERGVKLGDFIFYSVLVGKASATASGDMNTTACFAAILIGLCL 420
QY 421 TLLLLAIFKKALPALPISITFGLVFFAFADYLVQPMQDLAFHOFTI 467
Db 421 TLLLLAIFKKALPALPISITFGLVFFAFADYLVQPMQDLAFHOFTI 467

RESULT 10
AA018049
ID AA018049 standard; Protein; 467 AA.
AC AA018049;
XX
XX 02-SEP-2002 (first entry)
DT
XX
XX Presentilin protein.
DE
XX
XX Sel-12; presentilin; neuronal disorder; familial Alzheimer's disease;
KW amyloid precursor protein; APP.
KM
XX
XX OS Unidentified.
XX
XX US6376239-B1.
XX
XX 23-APR-2002.
XX
XX 04-APR-1997; 97US-0832867.
XX
XX 04-APR-1997; 97US-0832867.
XX
XX 04-APR-1997; 97US-0832867.
XX
XX (ELDG-) ELEGENE GMBH.
XX
XX Baumeister R;
XX
XX WPI; 2002-478281/51.
XX
XX DR N-PSDB; AAL47323.
XX
XX Isolated DNA molecule comprising promoter of the sel-12 gene from
PT Caenorhabditis elegans operably linked to heterologous gene, directs
PT expression in neural cells and is useful to develop drugs to treat
PT
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PT neuronal disorders -
XX
XX Claim 2; Fig 4; 78pp; English.
PS
XX
XX The present invention relates to DNA molecules comprising the promoter of
CC the sel-12 gene from Caenorhabditis elegans operably linked to a
CC heterologous DNA sequence encoding a protein of interest. The sequence
CC can be used to develop drugs for the treatment, prevention or delay of a
CC neuronal disorder. In particular, the neuronal protein may be familial
CC Alzheimer's disease. The present sequence is a presentilin protein
CC described in the exemplification of the invention.
XX
SQ Sequence 467 AA:
Query Match 99.8%; Score 2387; DB 23; Length 467;
Best Local Similarity 99.8%; Pred. No. 4.5e-235;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTELPAPLSYFQNAQMSSEDNHLSNTVRSQNDNERQEHNDRLSLGHPPLSNRPOGNSR 60
Db 1 MTELPAPLSYFQNAQMSSEDNHLSNTVRSQNDNERQEHNDRLSLGHPPLSNRPOGNSR 60
QY 61 QVVEODEEEDDELTKYGAHVIMLEVPVTLCAVVVVAATIKVSFETRKDGQLIYPTFE 120
Db 61 QVVEODEEEDDELTKYGAHVIMLEVPVTLCAVVVVAATIKVSFETRKDGQLIYPTFE 120
QY 121 DTEVVGORALHSLTNAIMISVIVMTILVLYKYRCYKVHIAWLISLLFFFSFI 180
Db 121 DTEVVGORALHSLTNAIMISVIVMTILVLYKYRCYKVHIAWLISLLFFFSFI 180
QY 181 YLGEVEKTYNAVDYITVALLIWNLGVMISIMHGKPLRLQOAYLIMISALMALVFIKY 240
Db 181 YLGEVEKTYNAVDYITVALLIWNLGVMISIMHGKPLRLQOAYLIMISALMALVFIKY 240
QY 241 LPETWAMLILAVISYDVAVLCRKPRLMLETQAERNETLPPALISSTWVLMNMAE 300
Db 241 LPETWAMLILAVISYDVAVLCRKPRLMLETQAERNETLPPALISSTWVLMNMAE 300
QY 301 GDEPAQRVSKNSKYNAESTERESODTVAENDDGFSEMEAROSHLGPHRSTPESRAA 360
Db 301 GDEPAQRVSKNSKYNAESTERESODTVAENDDGFSEMEAROSHLGPHRSTPESRAA 360
QY 361 VOELSSSIILAGEDPEERGVKLGDFIFYSVLVGKASATASGDMNTTACFAAILIGLCL 420
Db 361 VOELSSSIILAGEDPEERGVKLGDFIFYSVLVGKASATASGDMNTTACFAAILIGLCL 420
QY 421 TLLLLAIFKKALPALPISITFGLVFFAFADYLVQPMQDLAFHOFTI 467
Db 421 TLLLLAIFKKALPALPISITFGLVFFAFADYLVQPMQDLAFHOFTI 467

RESULT 11
AAU79416
ID AAU79416 standard; protein; 467 AA.
AC AAU79416;
XX
XX 02-JUL-2002 (first entry)
DT
XX
XX Human presentilin-1, PS-1.
DE
XX
XX Human; integrin-linked kinase; ILK; presentilin-1; protein kinase B; PKB;
KW gamma secretase; apoptosis; Alzheimer's disease; PS-1; neurotrophic;
KW neuroprotective; cytosstatic; cancer.
XX
XX Homo sapiens.
XX
XX WO200222862-A2.
XX
XX 21-MAR-2002.
XX
XX 12-SEP-2001; 2001WO-GB04094.
XX
```

PR 12-SEP-2000; 2000GB-0022333.

XX (GLAXO) GLAXO GROUP LTD.

XX Hiles ID, Ellis C;

XX WPI; 2002-351896/38.

XX Identifying agent that modulates interaction between integrin-linked
XX kinase and presentin-1, useful for treating Alzheimer's disease, and
XX identifying agent that modulates protein kinase B or gamma secretase
XX activity

PS Disclosure; Page 43-45; 53pp; English.

XX The invention relates to identifying an agent modulating interaction
XX between integrin-linked kinase (ILK) and presentin-1 (PS1) comprising
XX providing ILK, PS1 or their functional variants, as first and second
XX components respectively, contacting the components in the presence of
XX a test agent under conditions that in absence of the agent, would
XX permit the components to interact and determining whether the agent is
XX capable of modulating the interaction between the components. Also
XX included are the method above where the components are protein kinase
XX beta (PKB), gamma secretase or their functional variants, test kits
XX for carrying out the methods and an agent identified by the methods.
XX The methods are used for identifying an agent that modulates
XX interaction between ILK and PS1, or PKB or gamma-secretase. The agent has
XX therapeutic applications in treating humans or animals, for treating a
XX host suffering from a condition associated with an interaction between
XX ILK and PS1, activity of PKB, activity of gamma-secretase, apoptosis,
XX cancer and Alzheimer's disease. The agent is also useful for
XX manufacturing a medicament for use in treatment of the above mentioned
XX conditions. The present sequence represents human presentin-1, PS-1.

XX Sequence 467 AA:

Query Match 99.8%; Score 2387; DB 23; Length 467;

Best Local Similarity 99.8%; Pred. No. 4.5e-235;

Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFONAOQSEDNHLSNTVRSQNDNRERHNDRLSLGHPPLSGRPOGNSR 60
DB 1 MTELPAPLSYFONAOQSEDNHLSNTVRSQNDNRERHNDRLSLGHPPLSGRPOGNSR 60
QY 61 QVVEDDEDEDELTLKYGAKHYIMLFVPTLCMVVVAATIKSVSFTRKDGOLITTPPE 120
DB 61 QVVEDDEDEDELTLKYGAKHYIMLFVPTLCMVVVAATIKSVSFTRKDGOLITTPPE 120
QY 121 DRETVGORALHSILNAAIMISIVVMTILVLYKRYCYKVIHAWLISSLLLEFFSF 180
DB 121 DRETVGORALHSILNAAIMISIVVMTILVLYKRYCYKVIHAWLISSLLLEFFSF 180
QY 181 YLGEVFKTYNAVVDYITVALIMNIGVGMISIMHKGPIRLQOAYLIMSALMAVFIKY 240
DB 181 YLGEVFKTYNAVVDYITVALIMNIGVGMISIMHKGPIRLQOAYLIMSALMAVFIKY 240
QY 241 LPEMTAMILIAVSYDVAVLCPPKGPLMLVETAOERNETLFPALITSTVWVLYNMAE 300
DB 241 LPEMTAMILIAVSYDVAVLCPPKGPLMLVETAOERNETLFPALITSTVWVLYNMAE 300
QY 301 GDEPAORRVSKNSKYNAESTERESODTVAENDGGFSEMEARQDSHGLPHRSTPESRAA 360
DB 301 GDEPAORRVSKNSKYNAESTERESODTVAENDGGFSEMEARQDSHGLPHRSTPESRAA 360
QY 361 VOELSSSILAGDPREGRYKGLGDFIFYSVLYGKASATASGDWNTTACFVAAILGLCL 420
DB 361 VOELSSSILAGDPREGRYKGLGDFIFYSVLYGKASATASGDWNTTACFVAAILGLCL 420
QY 421 TLLLLAIFKKALPALPISTFGLVFYFATDYLVOPFMDLAHORFY 467
DB 421 TLLLLAIFKKALPALPISTFGLVFYFATDYLVOPFMDLAHORFY 467

RESULT 12

AAE17051

ID AAE17051 standard; Protein; 467 AA.

XX AAE17051;

XX 18-APR-2002 (first entry)

XX Human mutant presentin 1 (PS1) wild type protein.

KW Human; presentin 1; PS1; amyloid precursor protein; APP; drug screening;

KW Alzheimer's disease; Parkinson's disease; multiple sclerosis; stroke;

KW Huntington's disease; amyotrophic lateral sclerosis; Pick's disease;

KW head injury disease; frontal lobe dementia; cerebellar degeneration;

KW ischaemic injury; schizophrenia.

XX Homo sapiens.

XX WO200202601-A2.

XX 10-JAN-2002.

XX 29-JUN-2001; 2001WO-US16508.

XX 30-JUN-2000; 2000US-215345P.

XX (PHMA) PHARMACIA & UPJOHN CO.

XX Carter DB, Tomasselli AG;

XX WPI; 2002-140082/18.

PT Novel isolated mutant presentin 1 and presentin 2 polypeptides,
PT useful for screening of drugs for treating pathologies associated with
PT aberrant amyloid precursor protein processing, such as Alzheimer's
PT disease

PS Disclosure; Fig 1; 80pp; English.

CC The invention relates to mutant presentin 1 (PS1) and presentin 2
CC (PS2) polypeptides. Presentin are involved in the processing of amyloid
CC precursor protein (APP) from which major amyloidogenic peptides are
CC cleaved. Mutant presentins are useful for identifying agents that
CC modulate amyloid beta-peptide (Abeta) derived peptide production. Mutant
CC presentin is also useful as a target for screening drugs useful in the
CC treatment of pathologies associated with aberrant amyloid precursor
CC protein processing, such as Alzheimer's disease, Parkinson's disease,
CC multiple sclerosis, Huntington's disease, amyotrophic lateral sclerosis,
CC head injury disease, Pick's disease, frontal lobe dementia, cerebellar
CC degeneration, stroke, ischaemic injury and schizophrenia. A transgenic
CC non-human animal is useful for analysing the interaction between APP and
CC mutant presentin-1-processing protease in vivo, and for screening anti-
CC Alzheimer's disease drugs in vivo. A transgenic non-human
CC animal is useful for analysing the interaction between APP and mutant
CC presentin-1-processing protease in vivo, and for screening anti-
CC Alzheimer's disease drugs in vivo. The present sequence is human
CC PS1 wild type protein.

XX Sequence 467 AA:

Query Match 99.8%; Score 2387; DB 23; Length 467;

Best Local Similarity 99.8%; Pred. No. 4.5e-235;

Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFONAOQSEDNHLSNTVRSQNDNRERHNDRLSLGHPPLSGRPOGNSR 60
DB 1 MTELPAPLSYFONAOQSEDNHLSNTVRSQNDNRERHNDRLSLGHPPLSGRPOGNSR 60
QY 61 QVVEDDEDEDELTLKYGAKHYIMLFVPTLCMVVVAATIKSVSFTRKDGOLITTPPE 120
DB 61 QVVEDDEDEDELTLKYGAKHYIMLFVPTLCMVVVAATIKSVSFTRKDGOLITTPPE 120
QY 121 DRETVGORALHSILNAAIMISIVVMTILVLYKRYCYKVIHAWLISSLLLEFFSF 180

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|||||
Db 121 DFTVGORALHSLTNAIMISVIVMTILLVLYKRYCYKVIHAWLIISLLFFFSFI 180
QY 181 YLGEVFKTYNAVADYITVALINLGVGMISTHMKGPLRLQOAYLIMISALMALVFIRK 240
Db 181 YLGEVFKTYNAVADYITVALINLGVGMISTHMKGPLRLQOAYLIMISALMALVFIRK 240
QY 241 LPBMTAMLILAVISYVDLVAVLCPKGPLRLVETAQRNETLEPALIYSTWVLVNMME 300
Db 241 LPBMTAMLILAVISYVDLVAVLCPKGPLRLVETAQRNETLEPALIYSTWVLVNMME 300
QY 301 GDEAQRVRSKNSKYNAAESTERESQDTVAENDGGFSEMEARQDSHLGPHRSTPESRAA 360
Db 301 GDEAQRVRSKNSKYNAAESTERESQDTVAENDGGFSEMEARQDSHLGPHRSTPESRAA 360
QY 361 VOELSSIIAGDEPBERGVKLGDFIFYSVLVGKASATASGDMNTTICFAVAILIGLCL 420
Db 361 VOELSSIIAGDEPBERGVKLGDFIFYSVLVGKASATASGDMNTTICFAVAILIGLCL 420
QY 421 TLLLLAIFKKALPALPISITFGLVFFYFANDYLVQPMQDLAFHQFYI 467
Db 421 TLLLLAIFKKALPALPISITFGLVFFYFANDYLVQPMQDLAFHQFYI 467
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RESULT 13
AAW05755
ID AAW05755 standard; Protein; 467 AA.
AC AAW05755;
XX
DT 23-JUL-1997 (first entry)
XX
DE Presenilin-1-1 L286V mutation.
XX
KM Presenilin-1; human; hps1-1; hps1-2; PS-2; integral membrane protein; AD;
KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
XX depression; antibody; gene expression modulator; therapy; muten.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 286
FT /label= L286V
XX
PN W09634099-A2.
XX
PD 31-OCT-1996.
XX
PF 29-APR-1996; 96MO-CA00263.
XX
PR 31-JUL-1995; 95US-0509359.
PR 28-APR-1995; 95US-0431048.
PR 28-JUN-1995; 95US-0496841.
XX
PA (HSCR-) HSC RES & DEV LP.
PA (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
XX
PI Fraser PE, Rommens JM, St George-Hyslop PH;
XX
XX WPI; 1996-497631/49.
XX
PT New presenilin genes - useful for diagnosis, therapy and drug
XX screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
PS Claim 3; Page -; 178pp; English.
XX
CC AAW05736-W05760 represent mutated versions of the human presenilin-1-1
CC protein (see AAW05733 for wild type sequence). AAW05734 represents a
CC different wild type form of presenilin-1 that results from alternate
CC splicing of the genomic DNA sequence. The presenilins are a family of
CC highly conserved integral membrane proteins with a common structural
CC motif, common alternate splicing patterns, and common mutational hot
CC spot regions. Mutations in PS genes are implicated in familial
```

CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
CC haemorrhage, schizophrenia, depression etc., so detection of mutations in
CC the DNA encoding the wild type sequences can be used for diagnosis of
CC these diseases. The wild type proteins, or vectors that express them or
CC containing antisense sequences, antibodies selective for these mutant
CC forms of the proteins and modulators of PS gene expression are
CC potentially useful for treatment of AD etc. Transgenic animals are
CC useful as models for drug screening. The antibodies can also be used e.g.
CC for affinity purification and in immunoassays.

SO Sequence 467 AA;

Query Match 99.7%; Score 2384; DB 17; Length 467;

Best Local Similarity 99.6%; Pred. No. 9.2e-235;

Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MTELPAPLSYFONAKSEDNHLSNTVRSQNDNREORHNDRSGLHPEPLSNRPGNSR 60
Db 1 MTELPAPLSYFONAKSEDNHLSNTVRSQNDNREORHNDRSGLHPEPLSNRPGNSR 60
QY 61 QVEODEEDELTLKYGAKHVMLEFVPTLCMVVVAVATIKSVSEYTRKDGLIYPTPE 120
Db 61 QVEODEEDELTLKYGAKHVMLEFVPTLCMVVVAVATIKSVSEYTRKDGLIYPTPE 120
QY 121 DFTVGORALHSLTNAIMISVIVMTILLVLYKRYCYKVIHAWLIISLLFFFSFI 180
Db 121 DFTVGORALHSLTNAIMISVIVMTILLVLYKRYCYKVIHAWLIISLLFFFSFI 180
QY 181 YLGEVFKTYNAVADYITVALINLGVGMISTHMKGPLRLQOAYLIMISALMALVFIRK 240
Db 181 YLGEVFKTYNAVADYITVALINLGVGMISTHMKGPLRLQOAYLIMISALMALVFIRK 240
QY 241 LPBMTAMLILAVISYVDLVAVLCPKGPLRLVETAQRNETLEPALIYSTWVLVNMME 300
Db 241 LPBMTAMLILAVISYVDLVAVLCPKGPLRLVETAQRNETLEPALIYSTWVLVNMME 300
QY 301 GDEAQRVRSKNSKYNAAESTERESQDTVAENDGGFSEMEARQDSHLGPHRSTPESRAA 360
Db 301 GDEAQRVRSKNSKYNAAESTERESQDTVAENDGGFSEMEARQDSHLGPHRSTPESRAA 360
QY 361 VOELSSIIAGDEPBERGVKLGDFIFYSVLVGKASATASGDMNTTICFAVAILIGLCL 420
Db 361 VOELSSIIAGDEPBERGVKLGDFIFYSVLVGKASATASGDMNTTICFAVAILIGLCL 420
QY 421 TLLLLAIFKKALPALPISITFGLVFFYFANDYLVQPMQDLAFHQFYI 467
Db 421 TLLLLAIFKKALPALPISITFGLVFFYFANDYLVQPMQDLAFHQFYI 467

RESULT 14
AAW05758
ID AAW05758 standard; Protein; 467 AA.
AC AAW05758;
XX
DT 23-JUL-1997 (first entry)
XX
DE Presenilin-1-1 L392V mutation.
XX
KM Presenilin-1; human; hps1-1; hps1-2; PS-2; integral membrane protein; AD;
KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
XX depression; antibody; gene expression modulator; therapy; muten.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 392
FT /label= L392V
XX
PN W09634099-A2.
XX
PD 31-OCT-1996.
XX
```

PF 29-APR-1996; 96WO-CA00263.
 XX
 PR 31-JUL-1995; 95US-0509359.
 PR 28-APR-1995; 95US-0431048.
 PR 28-JUN-1995; 95US-0496841.
 XX
 PA (HSCR-) HSC RES & DEV LP.
 PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
 PI Fraser PE, Rommens JM, St George-Hyslop PH;
 WPI: 1996-497631/49.
 DR
 XX
 PT New presenilin genes - useful for diagnosis, therapy and drug
 PT screening of familial Alzheimer's disease, cerebral disorders, etc.
 XX
 PS Claim 3; Page -: 178pp; English.
 XX
 CC AAM05736-W05760 represent mutated versions of the human presenilin-1-1
 CC protein (see AAM05733 for wild type sequence). AAM05734 represents a
 CC different wild type form of presenilin-1 that results from alternate
 CC splicing of the genomic DNA sequence. The presenilins are a family of
 CC highly conserved integral membrane proteins with a common structural
 CC motif, common alternate splicing patterns, and common mutational hot
 CC spot regions. Mutations in PS genes are implicated in familial
 CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
 CC hemorrhage, schizophrenia, depression etc., so detection of mutations in
 CC the DNA encoding the wild type sequences can be used for diagnosis of
 CC these diseases. The wild type proteins, or vectors that express them or
 CC containing antisense sequences, antibodies selective for these mutant
 CC forms of the proteins and modulators of PS gene expression are
 CC potentially useful for treatment of AD etc. Transgenic animals are
 CC useful as models for drug screening. The antibodies can also be used e.g.
 CC for affinity purification and in immunoassays.
 XX
 SQ Sequence 467 AA;
 Query Match 99.7%; Score 2384; DB 17; Length 467;
 Best Local Similarity 99.6%; Pred. No. 9.2e-235;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MTELPAPLSTYFQNMQMSDNHLSNTVRSQNDNREOHENDRRSLGHPPLSNGRQGNR 60
 DB 1 MTELPAPLSTYFQNMQMSDNHLSNTVRSQNDNREOHENDRRSLGHPPLSNGRQGNR 60
 QY 61 QVVEODEDEDELTKYGAHVIMLFVPTLCMVVVAATIKSVSYTRKDDQLTYPTPE 120
 DB 61 QVVEODEDEDELTKYGAHVIMLFVPTLCMVVVAATIKSVSYTRKDDQLTYPTPE 120
 QY 121 DTEVVGQALHSINAAIMISIVVMTLLVLYKRCYKIHAMLITSSLLLEFFSFI 180
 DB 121 DTEVVGQALHSINAAIMISIVVMTLLVLYKRCYKIHAMLITSSLLLEFFSFI 180
 QY 181 YLGEVFKTYNAVDTYVALLIMNLGVVGMISIMHGKPLRLQOAVLIMISALMALVFITY 240
 DB 181 YLGEVFKTYNAVDTYVALLIMNLGVVGMISIMHGKPLRLQOAVLIMISALMALVFITY 240
 QY 241 YLGEVFKTYNAVDTYVALLIMNLGVVGMISIMHGKPLRLQOAVLIMISALMALVFITY 240
 DB 241 YLGEVFKTYNAVDTYVALLIMNLGVVGMISIMHGKPLRLQOAVLIMISALMALVFITY 240
 QY 241 LPEPTAMILLAVISVYDVAALCEKGPLRMVETRAQERNELFPALITSSIMWLVNNAE 300
 DB 241 LPEPTAMILLAVISVYDVAALCEKGPLRMVETRAQERNELFPALITSSIMWLVNNAE 300
 QY 301 GDPAPQRRVSKNSKYNAESTRESQDVAENDDGFSEMEAPQRSHLGPSPESRAA 360
 DB 301 GDPAPQRRVSKNSKYNAESTRESQDVAENDDGFSEMEAPQRSHLGPSPESRAA 360
 QY 361 VOELSSSTIAGEDPEERGVKLGDFIFYSVYVGKASATASGDMWTTTACFAVAILIGLCL 420
 DB 361 VOELSSSTIAGEDPEERGVKLGDFIFYSVYVGKASATASGDMWTTTACFAVAILIGLCL 420
 QY 421 TLLLLATFKKALPALPISITFGVLFYFATDYLQPFMOQLAFHOFYI 467
 DB 421 TLLLLATFKKALPALPISITFGVLFYFATDYLQPFMOQLAFHOFYI 467

RESULT 15
 AAM05737
 ID AAM05737 standard; Protein: 467 AA.
 XX
 AC AAM05737;
 XX
 DT 23-JUL-1997 (first entry)
 XX
 DE Presenilin-1-1 V82L mutation.
 XX
 XX Presenilin-1; human; hps1-2; ps-2; integral membrane protein; AD;
 KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
 KW depression; antibody; gene expression modulator; therapy; mutant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 82
 FT /label= V82L
 XX
 PN W09634099-A2.
 XX
 PD 31-OCT-1996.
 XX
 PD 29-APR-1996; 96WO-CA00263.
 PF
 XX
 PR 31-JUL-1995; 95US-0509359.
 PR 28-APR-1995; 95US-0431048.
 PR 28-JUN-1995; 95US-0496841.
 XX
 PA (HSCR-) HSC RES & DEV LP.
 PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
 PI Fraser PE, Rommens JM, St George-Hyslop PH;
 WPI: 1996-497631/49.
 DR
 XX
 PT New presenilin genes - useful for diagnosis, therapy and drug
 PT screening of familial Alzheimer's disease, cerebral disorders, etc.
 XX
 PS Claim 3; Page -: 178pp; English.
 XX
 CC AAM05736-W05760 represent mutated versions of the human presenilin-1-1
 CC protein (see AAM05733 for wild type sequence). AAM05734 represents a
 CC different wild type form of presenilin-1 that results from alternate
 CC splicing of the genomic DNA sequence. The presenilins are a family of
 CC highly conserved integral membrane proteins with a common structural
 CC motif, common alternate splicing patterns, and common mutational hot
 CC spot regions. Mutations in PS genes are implicated in familial
 CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
 CC hemorrhage, schizophrenia, depression etc., so detection of mutations in
 CC the DNA encoding the wild type sequences can be used for diagnosis of
 CC these diseases. The wild type proteins, or vectors that express them or
 CC containing antisense sequences, antibodies selective for these mutant
 CC forms of the proteins and modulators of PS gene expression are
 CC potentially useful for treatment of AD etc. Transgenic animals are
 CC useful as models for drug screening. The antibodies can also be used e.g.
 CC for affinity purification and in immunoassays.
 CC
 SQ Sequence 467 AA;
 Query Match 99.7%; Score 2384; DB 17; Length 467;
 Best Local Similarity 99.6%; Pred. No. 9.2e-235;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MTELPAPLSTYFQNMQMSDNHLSNTVRSQNDNREOHENDRRSLGHPPLSNGRQGNR 60
 DB 1 MTELPAPLSTYFQNMQMSDNHLSNTVRSQNDNREOHENDRRSLGHPPLSNGRQGNR 60
 QY 61 QVVEODEDEDELTKYGAHVIMLFVPTLCMVVVAATIKSVSYTRKDDQLTYPTPE 120
 DB 61 QVVEODEDEDELTKYGAHVIMLFVPTLCMVVVAATIKSVSYTRKDDQLTYPTPE 120

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QY 121 DRETGQRAHSLNNAIMISYIVWTLLVLYKYRCYKVIHAWLISSLLFFFSFI 180
DB 121 DRETGQRAHSLNNAIMISYIVWTLLVLYKYRCYKVIHAWLISSLLFFFSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLIWNIGVGMISIHMKGPLRLOOAYLIMTSALMALVFIRY 240
DB 181 YLGEVFKTYNVAVDYITVALLIWNIGVGMISIHMKGPLRLOOAYLIMTSALMALVFIRY 240
QY 241 LPEWTAMLLIAYISYDVAVLCPKGPLMVLVETAQERNETLEPALIYSSTWVLVNMAL 300
DB 241 LPEWTAMLLIAYISYDVAVLCPKGPLMVLVETAQERNETLEPALIYSSTWVLVNMAL 300
QY 301 GPEAQRVSKNSKYNAESTEREODTVAENDGGFSEMEARDSHLGPHRSTPESRAA 360
DB 301 GPEAQRVSKNSKYNAESTEREODTVAENDGGFSEMEARDSHLGPHRSTPESRAA 360
QY 361 VOELSSIIAGEDPERGKVLGLGDFIFYSVLVKASATASGDWNTTIACFYAILIGLCL 420
DB 361 VOELSSIIAGEDPERGKVLGLGDFIFYSVLVKASATASGDWNTTIACFYAILIGLCL 420
QY 421 TLLLLAIFKKALPALPISTFGIVFEFATDYLVOPEMDLAFHOFYI 467
DB 421 TLLLLAIFKKALPALPISTFGIVFEFATDYLVOPEMDLAFHOFYI 467

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